

Table 1

EAA (essential amino acids)		NEAA (non-essential amino acids)	
L-arginine·HCl	126.4 mg/l	L-alanine	8.9 mg/l
L-cystine	24.02 mg/l	L-asparagine	13.2 mg/l
L-histidine·HCl·H ₂ O	41.92 mg/l	L-aspartic-acid	13.3 mg/l
L-isoleucine	52.46 mg/l	L-glutamic acid	14.7 mg/l
L-leucine	52.46 mg/l	glycine	7.5 mg/l
L-lysine·HCl	73.06 mg/l	L-prolin	11.5 mg/l
L-methionine	14.92 mg/l	L-serine	10.5 mg/l
L-phenylalanine	33.02 mg/l		
L-threonine	47.64 mg/l		
L-tryptophane	10.2 mg/l		
L-tyrosine	36.22 mg/l		
L-valine	46.86 mg/l		

Single amino acids	
histidine·HCl·H ₂ O	20 mg/l
isoleucine	50 mg/l
leucine	50 mg/l
methionine	15 mg/l
phenylalanine	15 mg/l
threonine	20 mg/l
tyrosine	20 mg/l
arginine·HCl	240 mg/l
lysine	40 mg/l
D-lysine	40 mg/l
cystine	50 mg/l
tryptophane	5 mg/l
valine	20 mg/l
glutamine	300 mg/l

Table 2. APIT kills different tumor cell lines

models for	kind of tumor	tumor cell line	IC50 (ng/ml)
1. solid tumors	lung cancer	GLC4	9
	breast cancer	MCF-7, SK-BR-3	*
	prostate cancer	PC3, DU145	*
	colon cancer	HT-29	20
	cervix cancer	HeLa, Chang	*, 10
	uterus carcinoma	Hec-1-B	*
	larynx cancer	HEp-2	*
	stomach cancer	AGS	*
	liver cancer	Hep G2	*
2. leukemia	T cell leukemia (ALL)	Jurkat neo	3.2
	T cell leukemia (ALL)	CEM neo	5.6
	B cell leukemia	SKW neo	3
	Monocyte leukemia (AML)	Mono Mac 6	*
	Monocyte leukemia (AML)	THP-1	10
3. "orphan" tumors	Ewings sarcoma	RDES	4.5
		A673	5
4. apoptosis resistant tumors	(CML)	K562	4.25
	T cell leukemia (ALL)	Jurkat Bcl-2	2.7
	T cell leukemia (ALL)	CEM Bcl-XL	4.0
	B cell leukemia	SKW Bcl-2	5.5
5. MDR tumors	Lung cancer	GLC4-ADR	10

Table 3. Proteome analysis

Description	gi	NCBI	NCBI version	swissprot	effect
Aldolase A (E.C.4.1.2.13)	229674	1ALD	1ALD	P04075	-
26S proteasome regulatory chain 12	2134660	S65491	S65491	-	-
3-Hydroxyacyl-CoA dehydrogenase	2078327	AAB54008	AAB54008.1	Q16836	-
C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase)	115206	P11586	P11586	P11586	-
Chain A, Structure Of Human Glutamate Dehydrogenase-Apo Form or Glutamate dehydrogenase 1	20151189 4885281	1L1F_A NP_005262	1L1F_A NP_005262.1	- P00367	m
Cleavage and polyadenylation specific factor 5, 25 kD subunit	5901926	NP_008937	NP_008937.1	-	+
Cofilin 1	5031635	NP_005498	NP_005498.1	P23528	-
Coronin, actin binding protein, 1A	5902134	NP_009005	NP_009005.1	P31146	+
Dihydropyrimidine dehydrogenase precursor; E3 component of pyruvate dehydrogenase	4557525	NP_000099	NP_000099.1	P09622	-
dJ553F4.4 (Novel protein similar to Drosophila CG8055 protein)	12314022	CAC14088	CAC14088.1	-	+
DNA replication licensing factor MCM4	1705520	-	-	P33991	+
Elongation factor1-delta (EF-1-delta)	20141357	P29692	P29692	P29692	-
Enolase 1, alpha; phosphopyruvate hydratase	4503571	NP_001419	NP_001419.1	Q05524	+
Glyceraldehyde-3-phosphate dehydrogenase or uracil DNAGlycosylase	31645 35053	CAA25833 CAA37794	CAA25833.1 CAA37794.1	P04406* P04406*	+
Heat shock 60kD protein 1 (chaperonin)	14603309	AAH10112	AAH10112.1	Q96FZ6	-
Heat shock 60kDa protein 1 (chaperonin)	4504521	NP_002147	NP_002147.1	P10809	-
Heat shock 70kD protein 9B (mortalin-2)	4758570	NP_004125	NP_004125.1	Q8N1C8	-
Heterogeneous nuclear ribonucleoprotein C, isoform b	4758544	NP_004491	NP_004491.1	P07910	m
Hspc117	6841456	AAF29081	AAF29081.1	Q9P037	m
Inosine-5'-monophosphate dehydrogenase 2 (IMP dehydrogenase 2)	124419	P12268	P12268	P12268	+
Isocitrate dehydrogenase 3 (NAD+) alpha	5031777	NP_005521	NP_005521.1	P50213	-
KH-type splicing regulatory protein (FUSE binding protein 2)	4504865	NP_003676	NP_003676.1	-	-
Nuclear matrix protein NMP200 related to splicing factor PRP19	7657381	NP_055317	NP_055317.1	Q9UMS4	-
Nucleobindin 2	4826870	NP_005004	NP_005004.1	P80303	-
54 kDa nuclear RNA- and DNA-binding protein (p54(nrb)) (p54nrb)	13124797	Q15233	Q15233	Q15233	+
Peroxiredoxin 1 (Thioredoxin peroxidase 2)	548453	Q06830	Q06830	Q06830	m
Peroxiredoxin 1; Proliferation-associated gene A; proliferation-associated gene A	4505591	NP_002565.1	NP_002565.1	Q06830	m

Table 3. Continuation I

Description	gi	NCBI	NCBI version	swissprot	effect
Peroxioredoxin 2 (Thioredoxin peroxidase 1)	2507169	P32119	P32119	P32119	+
Peroxioredoxin 3; antioxidant protein 1; thioredoxin-dependent peroxide reductase precursor	5802974	NP_006784	NP_006784.1	P30048	-
2-phosphopyruvate-hydratase alpha-enolase; carbonate dehydratase	693933	CAA59331	CAA59331.1	P06733	+
Proteasome subunit alpha type 7	12643540	O14818	O14818	O14818	+
Proteasome subunit beta type 1 (Proteasome component C5) (Macropain subunit C5)	130853	P20618	P20618	P20618	+
Ras-GTPase-activating protein SH3-domain-binding protein; GAP binding protein	5031703	NP_005745.1	NP_005745.1	Q13283	m
Replication protein A2, 32kDa	4506585	NP_002937	NP_002937.1	P15927	-
Rho GDP-dissociation inhibitor 2 (Rho GDI beta) (Ly-GDI)	1707893	P52566	P52566	P52566	-
Ribosomal protein P0; 60S acidic ribosomal protein P0 or similar BLOCK 23	4506667	NP_000993	NP_000993.1	P05388	-
	20536934	XP_165448	XP_165448.1	Q8NHW5	
Ribosomal protein, large, P0	12654583	AAH01127	AAH01127.1	P05388	-
RNA-binding protein regulatory subunit	6005749	NP_009193	NP_009193.1	O14805	+
RNA-binding protein regulatory subunit	12720028	XP_001707	XP_001707.2	O14805	+
Semenogelin I; Semenogelin	4506883	NP_002998	NP_002998.1	P04279	-
Similar to villin 2 (ezrin)	15530243	AAH13903	AAH13903.1	P15311	-
Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	4826998	NP_005057	NP_005057.1	P23246	-
Stathmin 1; metablastin; prosolin; oncoprotein 18; phosphoprotein 19; leukemia-associated phosphoprotein-p18	5031851	NP_005554	NP_005554.1		-
U2 small nuclear ribonucleoprotein A' (U2 snRNP-A')	134094	P09661	P09661	P09661	+
Vimentin	4507895	NP_003371	NP_003371.1	P08670	-
Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2)	1172554	P45880	P45880	P45880	-

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Table 4. Transcriptome analysis

Unigene cluster	Description	GENE	gi	pir/NCBI/swissprot	effect
Hs.3833	3'-phosphoadenosine 5'-phosphosulfate synthase 1	PAPSS1	4885537	NP_005434.1	-
Hs.166563	replication factor C (activator 1) 1, 145kDa	RFC1	15011931	ref:NP_002904.2	-
Hs.78991	DNA segment, numerous copies, expressed probes (GS1 gene)	DXF68S1E	6912346	ref:NP_036212.1	-
Hs.326035	early growth response 1	EGR1	119242	sp:P18146	++
Hs.108885	collagen, type VI, alpha 1	COL6A1	15011913	ref:NP_001839.1	++
Hs.78944	regulator of G-protein signalling 2, 24kDa	RGS2	2135146	pir:I53020	++
Hs.110571	growth arrest and DNA-damage-inducible, beta	GADD45B	9945332	ref:NP_056490.1	++
Hs.78465	v-jun sarcoma virus 17 oncogene homolog (avian)	JUN	135298	sp:P05412	+
Hs.82646	DnaJ (Hsp40) homolog, subfamily B; member 1	DNAJB1	1706473	sp:P25685	+
Hs.169840	TTK protein kinase	TTK	346403	pir:A42861	+
Hs.211601	mitogen-activated protein kinase kinase kinase 12	MAP3K12	18202489	sp:Q12B52	+
Hs.345728	suppressor of cytokine signaling 3	SSI-3	4507235	ref:NP_003946.1	+
Hs.3776	zinc finger protein 216	ZNF216	5174755	ref:NP_005998.1	+
Hs.73037	cannabinoid receptor 2 (macrophage)	CNR2	450068	prf:1920360A	+
Hs.167578	EST, FLJ25357 hypothetical protein FLJ25357		740170	2004399A	+
Hs.8715	hypothetical protein MGC3232	MGC3232	3024681	sp:O00268	+
Hs.74520	spinocerebellar ataxia 1 (olivopontocerebellar ataxia 1, autosomal dominant, ataxin 1)	SCA1	1082237	pir:S46268	+
Hs.6151	pumilio homolog 2 (Drosophila)	PUM2	14277945	pdb:1IB3	+
Hs.8026	EST, Highly similar to SES2_HUMAN Sestrin 2 [H.sapiens]		13633882	sp:P58004	+
Hs.82173	TGFB Inducible early growth response	TIEG	11387050	sp:Q13118	+
Hs.198307	von Hippel-Lindau binding protein 1	VBP1	4507873	ref:NP_003363.1	+
Hs.179982	tumor protein p53-binding protein	TP53BPL	5032191	ref:NP_005793.1	+
Hs.2549	adrenergic, beta-3-, receptor	ADRB3	1070630	pir:QRHUBE	+
Hs.2128	dual specificity phosphatase 5	DUSP5	12707566	ref:NP_004410.2	+
Hs.36927	heat shock 105kD	HSP105B	5729879	ref:NP_006635.1	+
Hs.77558	high mobility group nucleosomal binding domain 3	HMGN3	2495254	sp:Q15651	+
Hs.460	activating transcription factor 3	ATF3	88875	pir:C34223	+
Hs.104125	adenylyl cyclase-associated protein	CAP	399184	sp:Q01518	+
Hs.24719	modulator of apoptosis 1	MAP-1	11545896	ref:NP_071434.1	+
Hs.8257	cytokine inducible SH2-containing protein	CISH	13124022	sp:Q9NSE2	+
Hs.101383	ESTs, Weakly similar to A43932 mucin 2 precursor, Intestinal - human (fragments)		2135765	pir:A43932	+

Table 4. Continuation I

Unigene cluster	Description	GENE	gi	pltr/NCBI/swissprot effect
Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	CDW52	4502761	ref:NP_001794.1 +
Hs.8084	hypothetical protein dJ465N24.2.1	DJ465N24.2.1	10092679	ref:NP_064713.1 +
Hs.78829	ubiquitin specific protease 10	USP10	11360280	pir:T47164 +
Hs.889	Charot-Leyden crystal protein	CLC	1942631	pdb:1LCL +
Hs.277401	bromodomain adjacent to zinc finger domain, 2A	BAZ2A	7304921	ref:NP_038477.1 +
Hs.300863	lethal (3) malignant brain tumor (3)mbt protein (Drosophila) homolog	H-L(3)MBT	14141728	ref:NP_056293.2 +
Hs.4552	ubiquitin 2	UBQLN2	16753207	ref:NP_038472.2 +
Hs.151903	GrpE-like protein cochaperone	HMGE	18202951	sp:Q9HAV7 +
Hs.36606	EST, Weakly similar to T29982 hypothetical protein F11G11.12 - [C. elegans]			+ +
Hs.85302	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)	ADARB1	2829669	sp:P78563 +
Hs.113823	ClpX caseinolytic protease X homolog (E. coli)	CLPX	14916956	sp:O76031 +
Hs.25911	HLA-B associated transcript 2	BAT2	18375626	ref:NP_542417.1 +
Hs.95821	osteoclast stimulating factor 1	OSTF1	11134088	sp:Q92882 +
Hs.11217	KIAA0877 protein	KIAA0877		+ +
Hs.301064	arfaptin 1	HSU52521	1703203	sp:P53367 +
Hs.276238	EST, Moderately similar to kinase suppressor of ras [Mus musculus]			+ +
Hs.211569	G protein-coupled receptor kinase 5	GPRK5	2135145	pir:A48277 +
Hs.25524	protein tyrosine phosphatase, non-receptor type 23	PTPN23	7512735	pir:T14756 +
Hs.94498	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	LILRA2	5803068	ref:NP_006857.1 +
Hs.24427	DKFZP566O1646 protein	DC8	7512839	pir:T08737 +
Hs.46	platelet-activating factor receptor	PTAFR	107346	pir:A40191 +
Hs.90800	EST, Highly similar to matrix metalloproteinase 16, isoform 1; membrane-type matrix metalloproteinase 3; membrane-type-3 matrix metalloproteinase [Homo sapiens]		13027802	ref:NP_005932.2 +
Hs.81648	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4	FLJ11021	2833266	sp:Q15696 +
Hs.80338	Bcl-2-associated transcription factor	BTF	7661958	ref:NP_055554.1 +
Hs.238407	EST, Weakly similar to hypothetical protein FLJ20489 [Homo sapiens] [H.sapiens]		8923452	ref:NP_060312.1 +
Hs.154668	KIAA039' gene product	KIAA0391	3024899	sp:O15091 +
Hs.76666	chromosome 9 open reading frame 10	C9orf10	13431358	sp:Q9NZB2 +
Hs.9701	growth arrest and DNA-damage-inducible, gamma	GADD45G	5729836	ref:NP_006696.1 +
Hs.100527	connector enhancer of KSR2	CNK2	7662368	ref:NP_055742.1 +
Hs.77274	plasminogen activator, urokinase	PLAU	224665	prf:1110198A +

Table 4. Continuation II

Unigene cluster	Description	GENE	gi	pir/NCBI/swissprot	effect
Hs.93516	ESTs				+
Hs.376709	Homo sapiens cDNA FLJ33768 fis, clone BRHIP2000021				+
Hs.110299	mitogen-activated protein kinase 7	MAP2K7	4826946	ref:NP_005034.1	+
Hs.31396	ESTs, Weakly similar to S28807 collagen alpha 1(X) chain precursor [M.musculus]				+
Hs.129715	gonadotropin-releasing hormone 2	GNRH2	3913735	sp:O43555	+
Hs.169370	FYN oncogene related to SRC, FGR, YES	FYN	125370	sp:P06241	+
Hs.82007	methionyl aminopeptidase 1	METAP1	1703270	sp:P53582	+
Hs.239018	RAB11B, member RAS oncogene family	RAB11B	1082426	pir:JC2487	+
Hs.126852	solute carrier family 6 (neurotransmitter transporter, GABA), member 13	SLC6A13	7705539	ref:NP_057699.1	+

Table 5. Transcriptome analysis

GENBANK	GENENAME	SYMBOL	EFFECT
NM_005252	v-fos FBJ murine osteosarcoma viral oncogene homolog	FOS	++
NM_006705	growth arrest and DNA-damage-inducible, gamma	GADD45G *	++
NM_001964	early growth response 1	EGR1 *	++
NM_002228	v-jun sarcoma virus 17 oncogene homolog (avian)	JUN *	++
NM_015675	growth arrest and DNA-damage-inducible, beta	GADD45B *	++
NM_001124	adrenomedullin	ADM	++
NM_005346	heat shock 70kDa protein 1B	HSPA1B	++
NM_002166	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	ID2	++
NM_004417	dual specificity phosphatase 1	DUSP1	++
NM_003745	suppressor of cytokine signaling 1	SOCS1	++
NM_002923	regulator of G-protein signalling 2, 24kDa	RGS2 *	++
NM_005627	serum/glucocorticoid regulated kinase	SGK	++
BC012321	activity-regulated cytoskeleton-associated protein	ARC	++
NM_025195	phosphoprotein regulated by mitogenic pathways	C8FW	+
NM_030751	transcription factor 8 (represses Interleukin 2 expression)	TCF8	+
NM_014330	protein phosphatase 1, regulatory (inhibitor) subunit 15A	PPP1R15A	+
NM_004083	DNA-damage-inducible transcript 3	DDIT3	+
NM_001841	cannabinoid receptor 2 (macrophage)	CNR2 *	+
NM_004024	activating transcription factor 3	ATF3 *	+
NM_001706	B-cell CLL/lymphoma 6 (zinc finger protein 51)	BCL6	+
NM_004428	ephrin-A1	EFNA1 *	+
NM_004419	dual specificity phosphatase 5	DUSP5 *	+
NM_003088	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	FSCN1	+
AB014566	dishvelled associated activator of morphogenesis 1	DAAM1	+
NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1	DNAJB1 *	+
NM_004962	growth differentiation factor 10	GDF10	+
D79994	kidney ankyrin repeat-containing protein	KANK	+
NM_006301	mitogen-activated protein kinase kinase kinase 12	MAP3K12 *	+
NM_002928	regulator of G-protein signalling 16	RGS16	+
NM_003955	suppressor of cytokine signaling 3	SOCS3	+
NM_004430	early growth response 3	EGR3	+
NM_001731	B-cell translocation gene 1, anti-proliferative	BTG1	+
NM_012342	putative transmembrane protein	NMA	+
NM_002262	killer cell lectin-like receptor subfamily D, member 1	KLRD1	+
NM_006007	zinc finger protein 216	ZNF216 *	+
NM_000905	neuropeptide Y	NPY	+

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Table 5. (continued) Transcriptome analysis						
GENBANK		GENENAME		SYMBOL	EFFECT	
NM_004418	dual specificity phosphatase 2			DUSP2	+	
NM_031459	sestrin 2			SES2	+	
AF332558	BCL2 binding component 3			BBC3	+	
NM_006000	tubulin, alpha 1 (testis specific)			TUBA1	+	
NM_006644	heat shock 105kDa/110kDa protein 1			HSPH1	+	
L24498	growth arrest and DNA-damage-inducible, alpha			GADD45A	+	
AK024029	modulator of apoptosis 1			MOAP1	+	
NM_005409	chemokine (C-X-C motif) ligand 11			CXCL11	+	
NM_003383	very low density lipoprotein receptor			VLDLR	+	
AF267856	hypothetical protein dJ465N24.2.1			DJ465N24.2.1A	+	
NM_002450	metallothionein 1L			MT1L	+	
NM_001828	Charot-Leyden crystal protein			CLC	+	
NM_013370	pregnancy-induced growth inhibitor			OKL38	+	
AB014581	l(3)mbt-like (Drosophila)			L3MBTL	+	
NM_006875	pim-2 oncogene			PIM2	+	
AL031665	actin, gamma pseudogene 3			ACTGP3	+	
A1985514	ribosomal protein S19			RPS19	+	
NM_080686	HLA-B associated transcript 2			BAT2	+	
NM_021184	chromosome 6 open reading frame 47			C6orf47	+	
NM_015471	DKFZP566O1646 protein			DC8	+	
NM_000952	platelet-activating factor receptor			PTAFR	+	
BC012625	protein phosphatase 1, regulatory (inhibitor) subunit 3C			PPP1R3C	+	
NM_023012	hypothetical protein FLJ11021 similar to splicing factor, arginine/serine-rich 4			FLJ11021	+	
AK024358	macrophage expressed gene 1			LOC219972	+	
NM_002658	plasminogen activator, urokinase			PLAU	+	
U12767	nuclear receptor subfamily 4, group A, member 3			NR4A3	+	
NM_016615	solute carrier family 6 (neurotransmitter transporter, GABA), member 13			SLC6A13	+	
NM_002135	nuclear receptor subfamily 4, group A, member 1			NR4A1	+	
AJ251595	CD44 antigen (homing function and Indian blood group system)			CD44	-	
NM_005433	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1			YES1	-	
NM_006325	RAN, member RAS oncogene family			RAN	-	
NM_004775	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6			B4GALT6	-	
AK056671	upstream regulatory element binding protein 1			UREB1	-	
NM_022817	period homolog 2 (Drosophila)			PER2	-	
L07044	calcium/calmodulin-dependent protein kinase (CaM kinase) II gamma			CAMK2G	-	
NM_014890	downregulated in ovarian cancer 1			DOC1	-	

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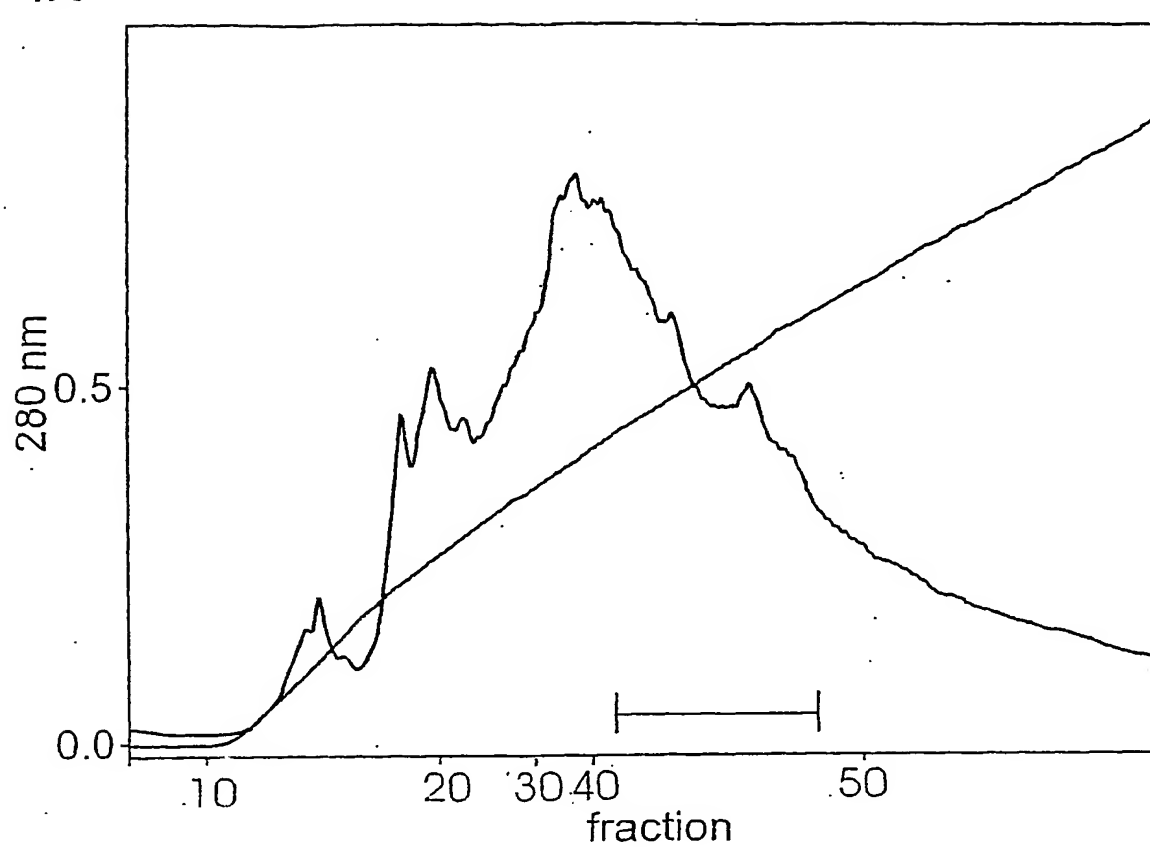
Table 5. (continued) Transcriptome analysis

GENBANK	GENENAME	SYMBOL	EFFECT
NM_001782	CD72 antigen	CD72	-
NM_005766	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	FARP1	-
NM_000566	Fc fragment of IgG, high affinity Ia, receptor for (CD64)	FCGR1A	-
NM_003036	v-ski sarcoma viral oncogene homolog (avian)	SKI	-
NM_001713	betaine-homocysteine methyltransferase	BHMT	-
NM_001682	ATPase, Ca++ transporting, plasma membrane 1	ATP2B1	-
NM_003985	tyrosine kinase, non-receptor, 1	TNKK1	-
NM_004752	glial cells missing homolog 2 (Drosophila)	GCM2	-
BC001619	aldehyde dehydrogenase 1 family, member B1	ALDH1B1	-
NM_002422	matrix metalloproteinase 3 (stromelysin 1, progelatinase)	MMP3	-
NM_003024	Intersectin 1 (SH3 domain protein)	ITSN1	-
NM_002613	3-phosphoinositide dependent protein kinase-1	PDPK1	-
NM_000098	carnitine palmitoyltransferase II	CPT2	-
BC002712	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian)	MYCN	-
NM_003112	Sp4 transcription factor	SP4	-
NM_012062	dynamitin 1-like	DNM1L	-
NM_000880	Interleukin 7	IL7	-
NM_004564	PET112-like (yeast)	PET112L	-
NM_001771	CD22 antigen	CD22	-
AA0904067	protein phosphatase 1, regulatory (inhibitor) subunit 12B	PPP1R12B	-
NM_001633	alpha-1-microglobulin/bikunin precursor	AMBIP	-
NM_007216	Hernansky-Pudlak syndrome 5	HPS5	-
AV705310	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	PPP2CA	-
AF296765	cerebral cavernous malformations 1	CCM1	-
AF155117	kinesin family member 21A	KIF21A	-
NM_002006	fibroblast growth factor 2 (basic)	FGF2	-
NM_004362	calmeglin	CLGN	-
NM_021221	lymphocyte antigen 6 complex, locus G5B	LY6G5B	-
AK001541	secretory carrier membrane protein 1	SCAMP1	-
H08291	acid phosphatase 1, soluble	ACP1	-
NM_014636	Ral guanine nucleotide exchange factor RalGPS1A	RALGPS1A	-
NM_053006	serine/threonine kinase 22B (spermiogenesis associated)	STK22B	-
NM_000220	potassium inwardly-rectifying channel, subfamily J, member 1	KCNJ1	-
NM_000633	B-cell CLL/lymphoma 2	BCL2	-
NM_003605	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	OGT	-

Table 5. (continued) Transcriptome analysis			SYMBOL	EFFECT
GENBANK	GENENAME			
NM_006114	translocase of outer mitochondrial membrane 40 homolog (yeast)		TOMM40	-
NM_013404	mesothelin		MSLN	-
NM_020974	signal peptide, CUB domain, EGF-like 2		SCUBE2	-
NM_000439	proprotein convertase subtilisin/kexin type 1		PCSK1	-
NM_002035	follicular lymphoma variant translocation 1		FVT1	-
AL136924	Ras and Rab interactor 2		RIN2	-
NM_006020	alkB, alkylation repair homolog (E. coli)		ALKBH	-
NM_005433	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1		YES1	-
NM_003423	zinc finger protein 43 (HTF6)		ZNF43	-
AF056490	phosphodiesterase 8A		PDE8A	-
NM_033480	F-box only protein 9		FBXO9	-
NM_022789	Interleukin 17E		IL17E	-
NM_007150	zinc finger protein 185 (LIM domain)		ZNF185	-
NM_017450	BAI1-associated protein 2		BAIAP2	-
AB037762	myelin expression factor 2		MYEF2	-
NM_003263	toll-like receptor 1		TLR1	-
NM_001089	ATP-binding cassette, sub-family A (ABC1), member 3		ABCA3	-
NM_018240	kin of IRRE like (Drosophila)		KIRREL	-
NM_003827	N-ethylmaleimide-sensitive factor attachment protein, alpha		NAPA	-
NM_003569	synixin 7		STX7	-
AB046797	KIAA1577 protein		KIAA1577	-
AV723914	hypothetical protein LOC164729		LOC164729	-
NM_015967	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)		PTPN22	-
AB007892	CDC5 cell division cycle 5-like (S. pombe)		CDC5L	-
NM_022907	hypothetical protein FLJ23053		FLJ23053	-
NM_004379	cAMP responsive element binding protein 1		CREB1	-
AB023198	KIAA0981 protein		KIAA0981	-
NM_024958	chromosome 20 open reading frame 98		C20orf98	-
NM_001186	BTB and CNC homology 1, basic leucine zipper transcription factor 1		BACH1	-
NM_014639	KIAA0372 gene product		KIAA0372	-
NM_024641	mannosidase, endo-alpha		MANEA	-
AK056671	upstream regulatory element binding protein 1		UREB1	-
NM_003618	mitogen-activated protein kinase kinase kinase 3		MAP4K3	-
NM_005443	3'-phosphoadenosine 5'-phosphosulfate synthase 1		PAPSS1	*
NM_022781	ring finger protein 38		RNF38	-
NM_003874	CD84 antigen (leukocyte antigen)		CD84	-

Table 5. (continued) Transcriptome analysis

GENBANK	GENENAME	SYMBOL	EFFECT
NM_000091	collagen, type IV, alpha 3 (Goodpasture antigen)	COL4A3	-
NM_000160	glucagon receptor	GCGR	-
NM_005019	phosphodiesterase 1A, calmodulin-dependent	PDE1A	-
NM_012080	family with sequence similarity 16, member A, X-linked	FAM16AX	-

Fig.
1A

1B

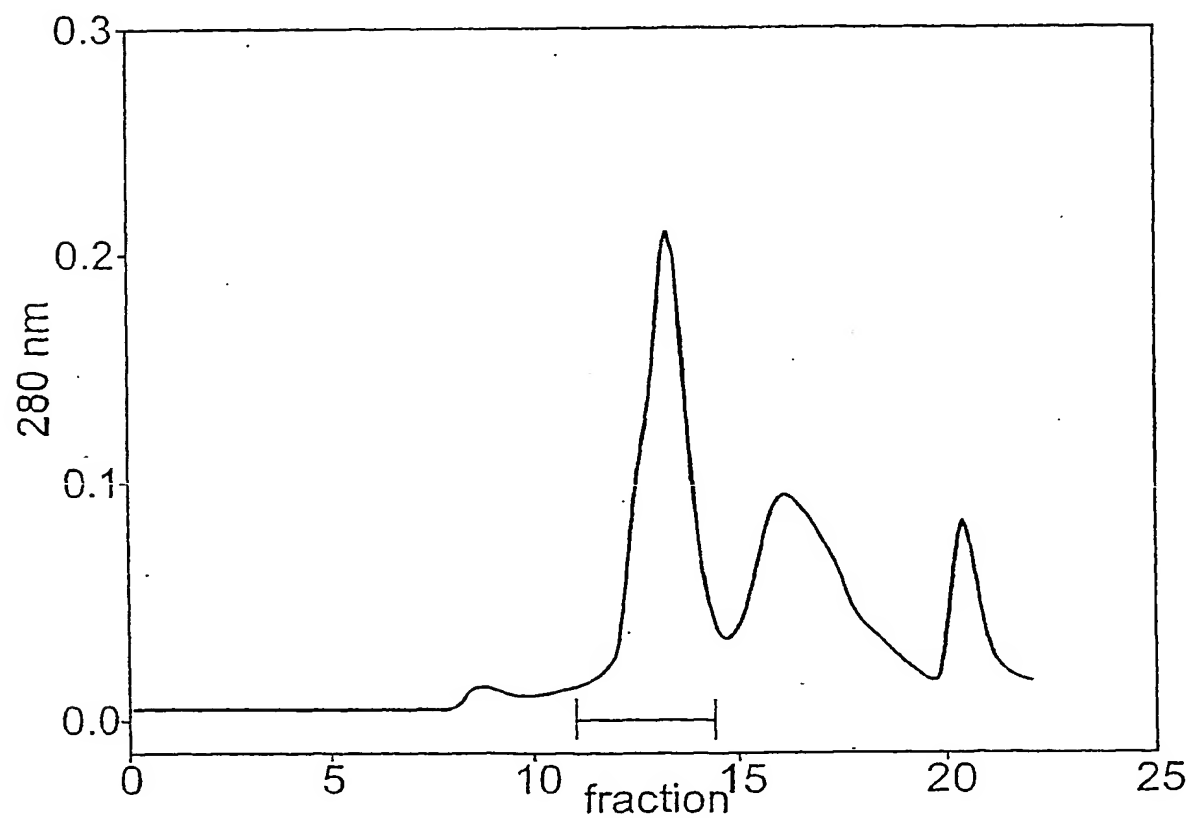


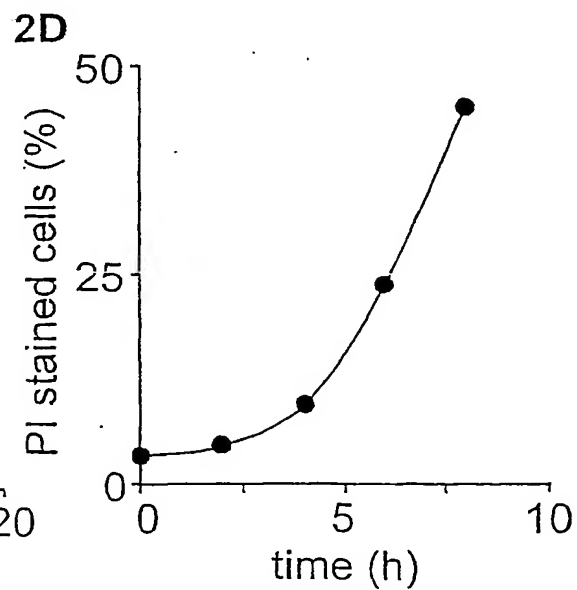
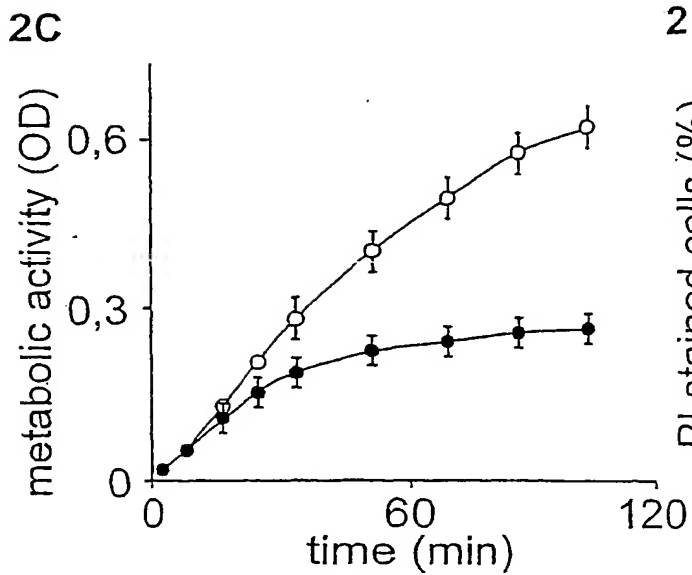
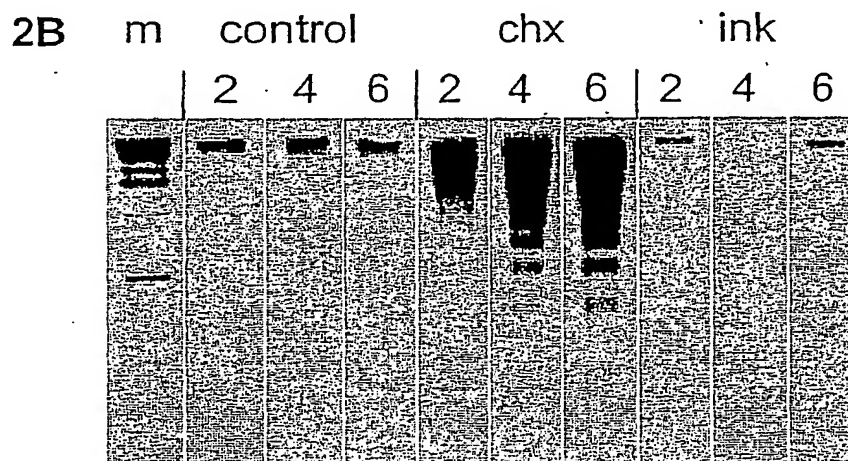
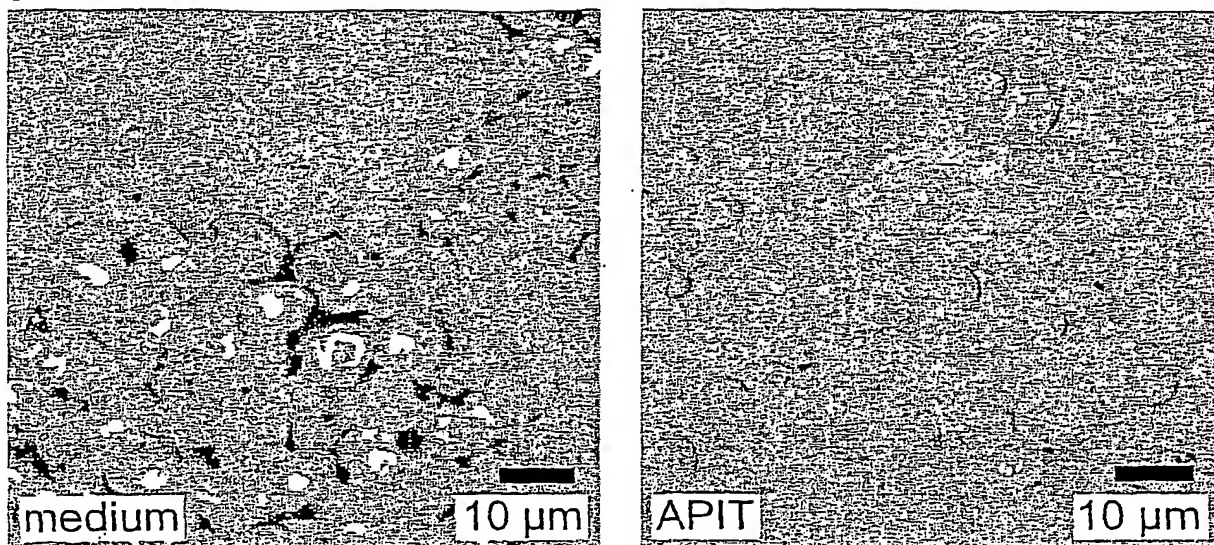
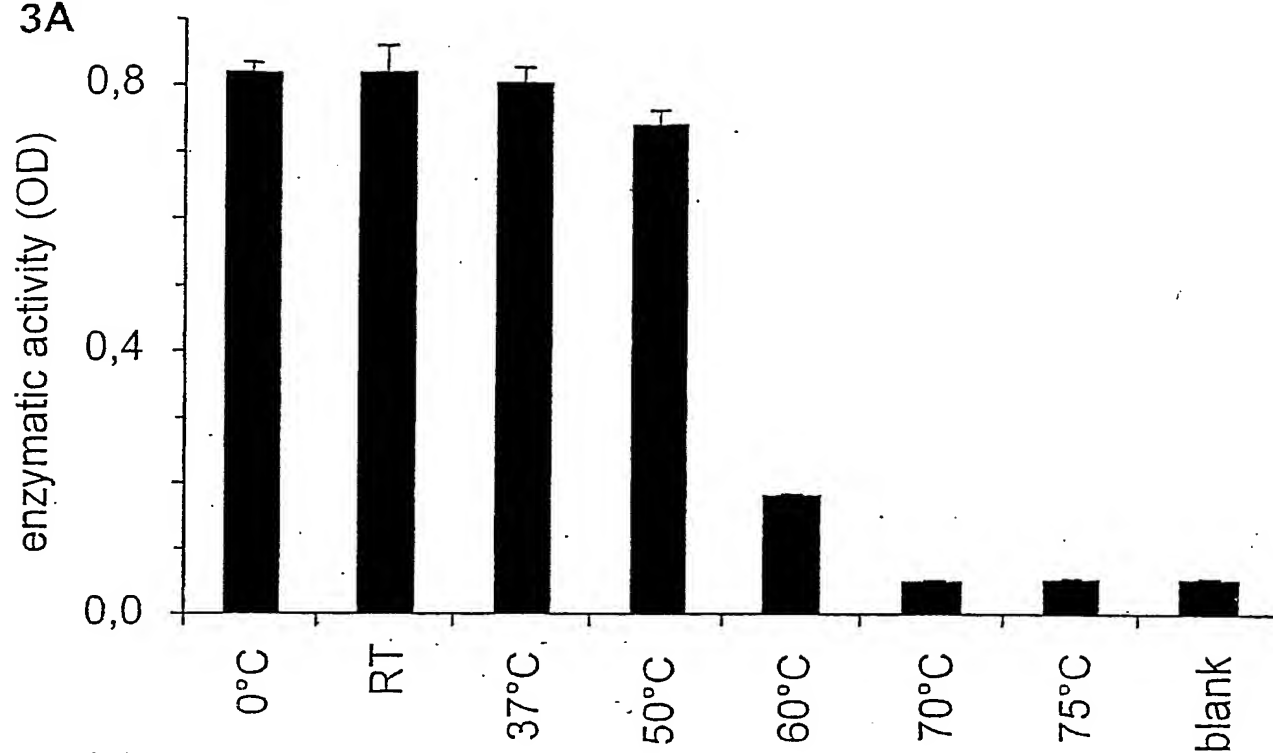
Fig.
2A

Fig.

3A



3B

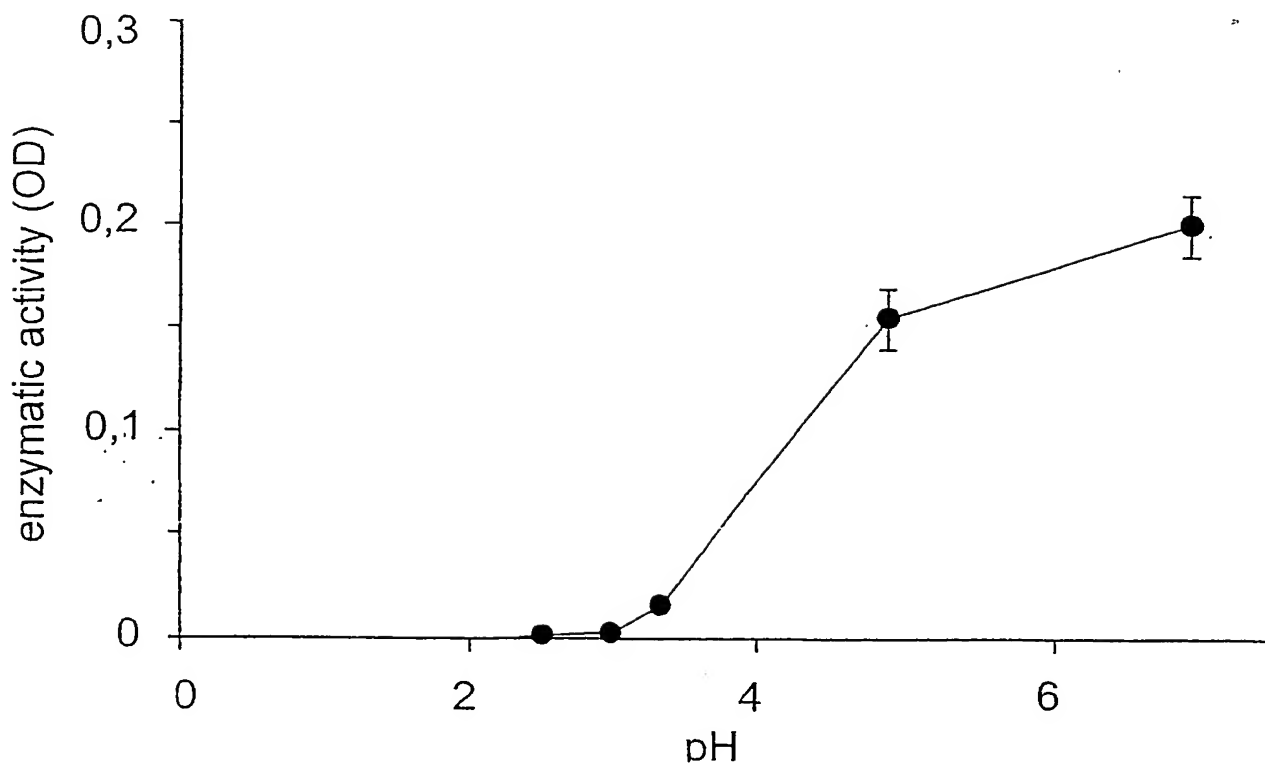


Fig.

3C

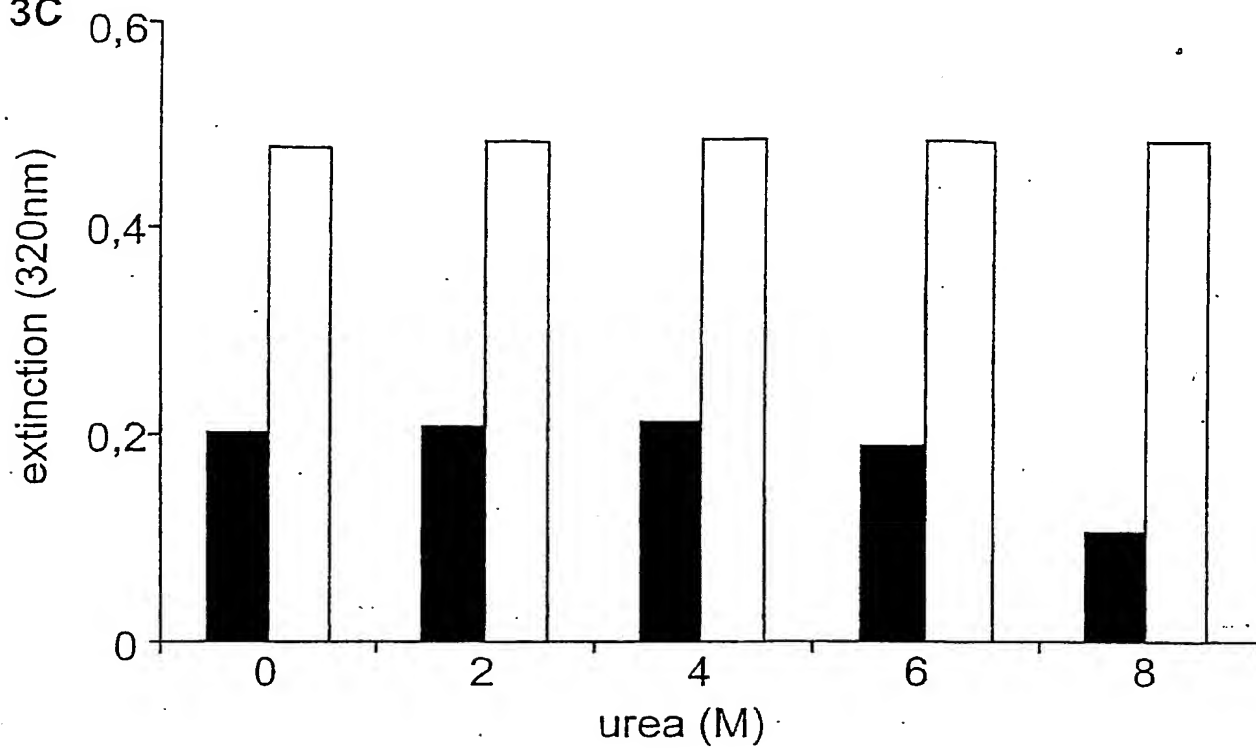


Fig.
4A

N-terminal sequence:

D-G-I-C-R-N-Q-R-Q
Q V R PInternal peptide sequences

	Sequence
1	DSGLDIA <u>VFEYS</u> DR
2	LFX YQLPNTPDVNLEI
3	VISELGLTPK
4	XGDVPYDLSPEEK
5	VILAXPVYALN
6	ATQAYAAVRPIPA SK
7	VFMTFDQP
8	SDALFFQMYD
9	SEASGDYILIASYADGLK
10	NQGEDIPGSDPQYNQVTEP(L)(K)

X = not determinable

underlined: primer sequence for RT-PCR

Fig.
4B

1	Oligo-dT DBuTag1	tcc taa cgt agg tct aga cct gtt gca ttt ttt ttt ttt ttt ttt
2	V-Fey 3 DTS 5'	tc gtg ttc gar tac tci gay cg
3	DBuTag1 DTS 3'	ctg tag gtc tag acc tgt tgc a
4	ATF Race 3' 660	ccg tgt aga tct cac tgc cat a
5	Abrided Anchor Primer	ggc cac gcg tcg act agt acg ggi igg gii ggg iig
6	ATF Race 3' 436	ccg ttg agt tgt aga cct
7	AUAP-EcoRI	aatt ggc cac gcg tcg act agt ac
8	ATF 5' Sign Eco RI GEX/ET	aa ttc tcg tct gct gtg ctt ctc ct
9	ATF 3' XhoI	gac tta gag gaa gta gtc gtt ga

Fig.

4C

M S S A V L L L A C A L V I S V H A D G IV C
ATGTCGTCTGCTGTGCTTCTCCTGGCTTGTGCGTTGGTCATCTCTGTCCACGCCGACGGTATCTGC
...TCGTCTGCTGTGCTTCTCCTGGCTTGTGCGTTGGTCATCTCTGTCCACGCCGACGGTCTCTGC
.....GACGGTATCTGC

R N R R Q C N R E V C G S T Y D V A V V G A
AGAAACAGACGTCAATGTAACAGAGAGGTGTGCGGTTCTACCTACGATGTGGCCGTCGTGGGGGCG
AGAAACAGACGTCAATGTAACAGAGAGGTGTGCGGTTCTACCTACGATGTGGCCGTCGTGGGGGCG
AGAAACAGACGTCAATGTAACAGAGAGGTGTGCGGTTCTACCTACGATGTGGCTGTCTGTGGGGGCG

G P G G A N S A Y M L R D S G L D I A V F E
GGGCCTGGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCCTGGACATCGCTGTGTTTCGAG
GGGCCTGGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCCTGGACATCGCTGTGTTTCGAG
GGGCCTGGGGGAGCTAACTCCGCCTACATGCTGAGGGACTCCGGCCTGGACATCGCTGTGTTTCGAG

Y S D R V G G R L F T Y O L P N T P D V N L
TACTCGGACCGAGTGGGCGGCCGGCTGTTACCTACCAGCTGCCCAACACACCCGACGTAACTCTG
TACTCAGACCGAGTGGGCGGCCGGCTGTTACCTACCAGCTGCCCAACACACCCGACGTAACTCTC
TACTCAGACCGAGTGGGCGGCCGGCTGTTACCTACCAGCTGCCCAACACACCCGACGTAACTCTC

E I G G M R F I E G A M H R L W R V I S E L
GAGATTGGCGGCATGAGGTTTCATCGAAGGCGCCATGCACAGGCTCTGGAGGGTCATTTTCAGAACTC
GAGATTGGCGGCATGAGGTTTCATCGAGGGCGCCATGCACAGGCTCTGGAGGGTCATTTTCAGAACTC
GAGATTGGCGGCATGAGGTTTCATCGAGGGCGCCATGCACAGGCTCTGGAGGGTCATTTTCAGAACTC

G L T P K V F K E G F G K E G R Q R F Y L R
GGCCTAACCCCAAGGTGTTCAAGGAAGGTTTCGGCAAGGAGGGGCAGACAGAGATTTTACCTGCGG
GGCCTAACCCCAAGGTGTTCAAGGAAGGTTTCGGAAAGGAGGGGCAGACAGAGATTTTACCTGCGG
GGCCTAACCCCAAGGTGTTCAAGGAAGGTTTCGGAAAGGAGGGGCAGACAGAGATTTTACCTGCGG

G Q S L T K K Q V K S G D V P Y D L S P E E
GGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAG
GGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAG
GGACAGAGCCTGACCAAGAAACAGGTCAAGAGTGGGGACGTACCCTATGACCTCAGCCCGGAGGAG

K E N Q G N L V E Y Y L E K L T G L QK L N G
AAAGAAAACCAGGGAAATCTGGTCGAATACTACCTGGAGAACTGACAGGTCTACAACTCAACGGC
AAAGAAAACCAGGGAAATCTGGTCGAATACTACCTGGAGAACTGACAGGTCTACAACTCAATGGT
AAAGAAAACCAGGGAAATCTGGTCGAATACTACCTGGAGAACTGACAGGTCTAACTCAACGGC

EG P L K R E V A L K L T V P D G R F L Y D L
GAGCCGCTCAAACGTGAGGTTGCGCTTAACTAACCCTGTCGGACGGCAGATTCTCTATGACCTC
GAACCGCTCAAACGTGAGGTTGCGCTTAACTAACCCTGTCGGACGGCAGATTCTCTATGACCTC
GAGCCGCTCAAACGTGAGGTTGCGCTTAACTAACCCTGTCGGACGGCAGATTCTCTATGACCTC

S F D E A M D L V A S P E G K E F T R D T H
TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCCTGAGGGCAAAGAGTTCACCCGAGACACGCAC
TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCCTGAGGGCAAAGAGTTCACCCGAGACACGCAC
TCGTTTGACGAAGCCATGGATCTGGTTGCCTCCCCTGAGGGCAAAGAGTTCACCCGAGACACGCAC

Fig.

4C (continued)

V F T G E V T L DG A S A V S L F D D H L G E
GTCTTCACAGGAGAGGTCACCCTGGACGCGTCGGCTGTCTCCCTCTTCGACGACCACCTGGGAGAG
GTCTTCACCGGAGAGGTCACCCTGGGCGCGTCGGCTGTCTCCCTCTTCGACGACCACCTGGGAGAG
GTGTTACCGGAGAAGTCACCCTGGACGCGTCGGCTGTCTCCCTCTTCGACGACCACCTGGGAGAG

D Y Y G S E I Y T L K E G L S S V P Q G L L
GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTTCCGTCCCACAAGGGCTCCTA
GACTACTACGGCAGTGAGATCTACACCCTCAAGGAAGGACTGTCTTCCGTCCCICAAGGGCTCCTA
GACTACTATGGCAGTGAGATCTACACCCTAAAGGAAGGACTGTCTTCCGTCCCACAAGGGCTCCTA

Q AT F L D A A D S N E F Y P N S H L K A L R
CAGGCTTTTCTGGACGCGCGAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA
CAGGCTTTTCTGGACGCGCGAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA
CAGACTTTTCTGGACGCGCGAGACTCCAACGAGTTCTATCCCAACAGCCACCTGAAGGCCCTGAGA

R K T N G Q Y V L Y F E P T T S K D G Q T T
CGTAAGACCAACGGTCAGTATGTTCTTTACTTTGAGCCCACCACCTCCAAGGATGGACAAACCACA
CGTAAGACCAACGGTCAGTATGTTCTTTACTTTGAGCCCACCACCTCCAAGGATGGACAAACCACA
CGTAAGACCAACGGTCAGTATGTTCTTTACTTTGAGCCCACCACCTCCAAGGATGGACAAACCACA

I N Y L E P L Q V V C A Q R V I L A M P V Y
ATCAACTATCTGGAACCCCTGCAGGTTGTGTGTGCACAAAGAGTCATCCTGGCCATGCCGGTATAC
ATCAACTATCTGGAACCCCTGCAGGTTGTGTGTGCACAGAGAGTCATTCTGGCCATGCCGGTCTAC
ATCAACTATCTGGAACCCCTGCAGGTTGTGTGTGCACAGAGAGTCATCCTGGGATGCCGGTCTAC

A L N Q L D W N Q L R N D R A T O A Y A A V
GCTCTGAACCAACTAGACTGGAATCAGCTCAGAAATGACCGAGCCACCCAAGCGTACGCTGCCGTT
GCTCTCAACCAGTGGATTTGGAATCAGCTCAGAAATGACCGAGCCACCCAAGCGTACGCTGCCGTG
GCTCTCAACCAACTGGACTGGAATCAGCTCAGAAATGACCGAGCCACCCAAGCGTACGCTGCCGTG

R P I P A S K V F M TS F D O P W W L E N E R
CGCCCGATTCTGCAAGTAAGGTGTTTCATGTCCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG
CGCCCGATTCTGCAAGTAAGGTGTTTCATGACCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG
CGCCCGATTCTGCAAGTAAAGTGTTTCATGACCTTTGATCAGCCCTGGTGGTTGGAGAACGAGAGG

K S W V T K S D A L F S O M Y D W Q K S E A
AAATCCTGGGTCACCAAGTCGGACGCGCTTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG
AAATCCTGGGTCACCAAGTCGGACGCGCTTTTCAGTCAAATGTACGACTGGCAGAAGTCTGAGGCG
AAATCCTGGGTCACCAAGTCGGACGCGCTTTTCAGCCAAATGTACGACTGGCAGAAGTCTGAGGCG

S G D Y I L I A S Y A D G L K A Q Y L R E L
TCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTG
TCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTG
TCCGGAGACTACATCCTGATCGCCAGCTACGCCGACGGCCTCAAAGCCCAGTACCTGCGGGAGCTG

K N O G E D I P G S D P G Y N O V T E P L K
AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTTACCGAACCCCTCAAG
AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTACCGAACCCCTCAAG
AAGAATCAGGGAGAGGACATCCCAGGCTCTGACCCAGGCTACAACCAGGTACCGAACCCCTCAAG

Fig.

4C (continued)

D T I L D H L T E A Y G V E R D S I PR E P V
 GACACCATTCTTGACCACCTCACTGAGGCTTATGGCGTGGAGCGAGACTCGATCCCGGAACCCGTG
 GACACCATTCTTGACCACCTCACTGAGGCTTATGGCGTGGAGCGAGACTCGATCCCGGAACCCGTG
 GACACCATTCTTGACCACCTCACTGAGGCTTATGGCGTGGAGCGAGACTCGATCCCGGAACCCGTG

T A A S Q F W T D Y P F G C G W I T W R A G
 ACCGCCGCTTCCCAGTTCTGGACAGACTACCCGTTTGGCTGTGGATGGATCACCTGGAGGGCCGGC
 ACCGCCGCTTCCCAGTTCTGGACAGACTACCCGTTTGGCTGTGGATGGATCACCTGGAGGGCCGGC
 ACCGCCGCTTCCCAGTTCTGGACGACTACCCGTTTGGCTGTGGATGGATCACCTGGAGGGCCGGC

F H F D D V I S T M R R P S L K D E V Y V V
 TTCCATTTTCGATGACGTCATCAGCACCATGCGTCGCCCCGTCACTGAAAGATGAGGTATACGTGGTG
 TTCCATTTTCGATGACGTCATCAGCACCATGCGTCGCCCCGTCACTGAAAGATGAGGTCTACGTGGTG
 TTCCATTTTCGATGACGTCATCAGCACCATGCGTCGCCCCGTCACTGAAAGATGAGGTCTACGTGGTG

G A D Y S W G L I S S W I E G A L E T S E N
 GGAGCCGATACTCCTGGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC
 GGAGCCGATACTCCTGGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC
 GGAGCCGATACTCCTGGGGACTTATCTCCTCCTGGATAGAGGGCGCTCTGGAGACCTCGGAAAAC

V I N D Y F L -
 GTCATCAACGACTACTTCCTCTAA
 GTCATCAACGACTACTTCCTCTAA
 GTCATCAACGACTACTTCCTCTAA

4D

VS

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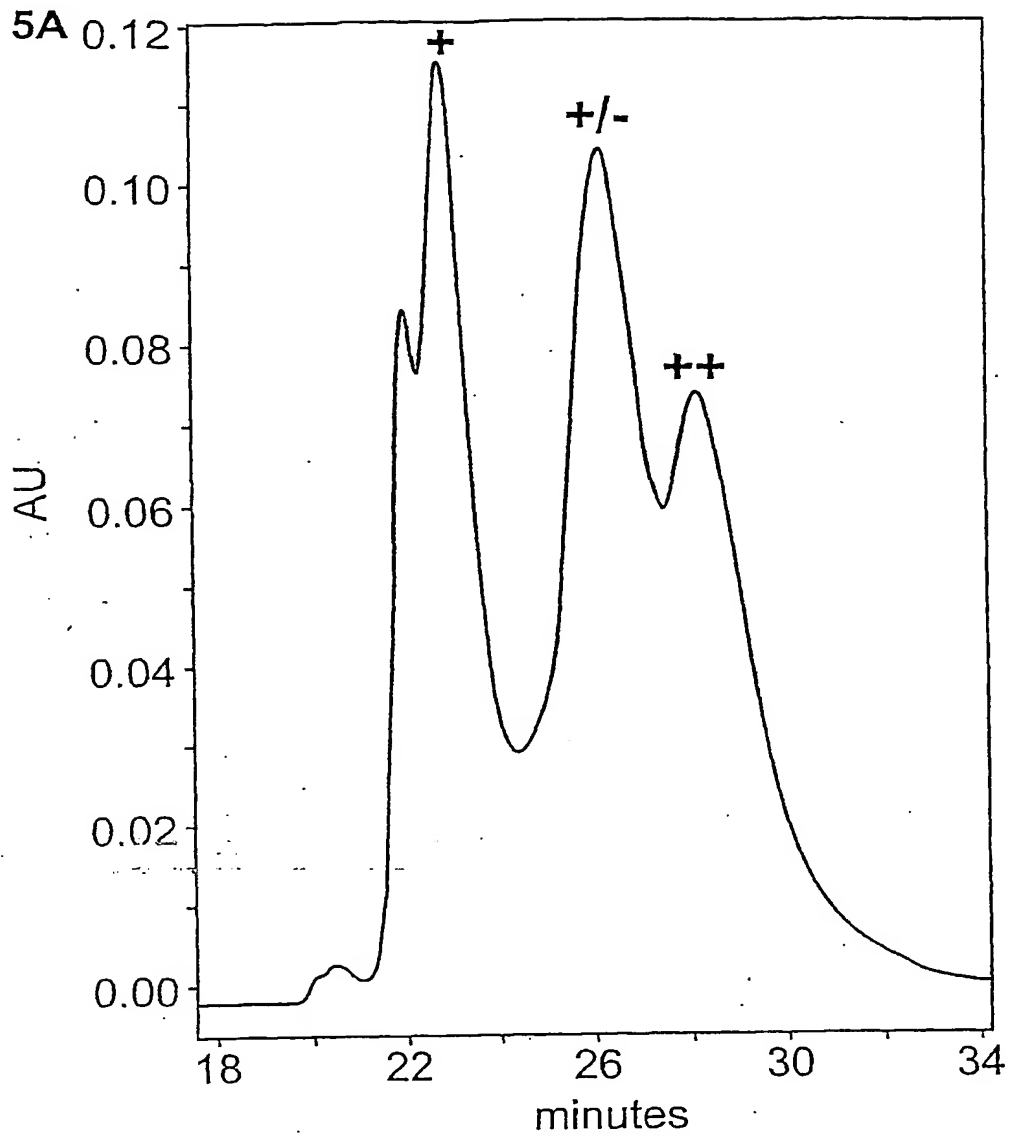
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T Q H S

GPGGANSAYMLRDSGLDIAVFEYSDRVGGRLFTIYQLPNTPDVNL

50 60 70 80

Fig.



5B

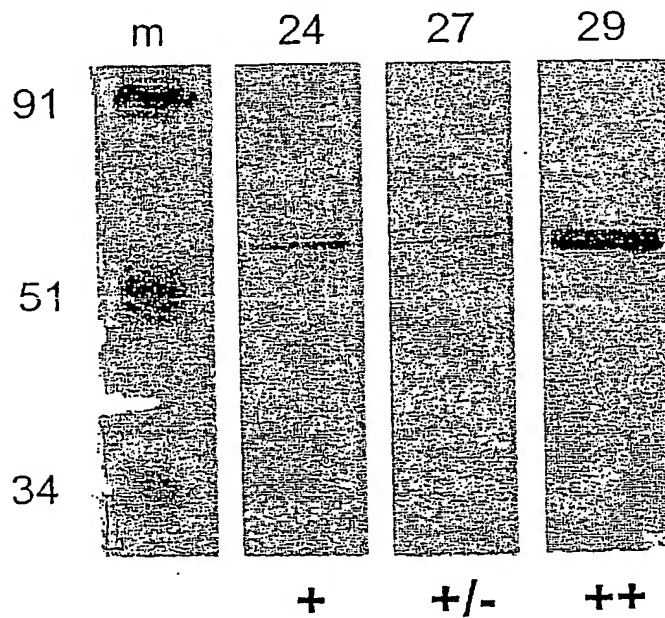


Fig.

5 C

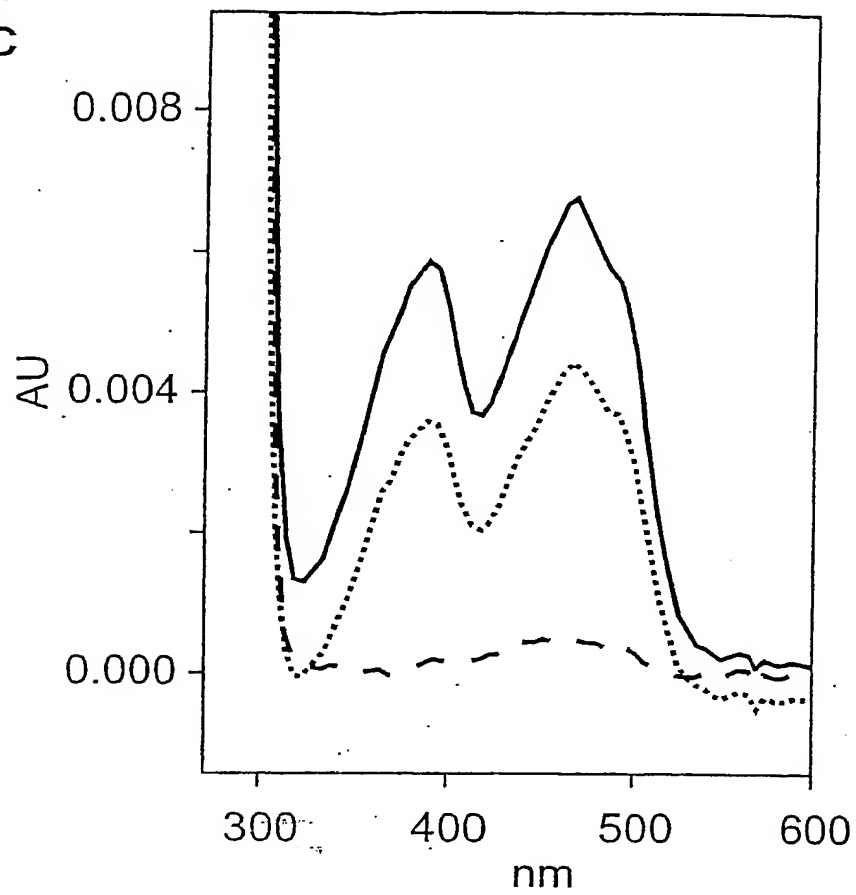
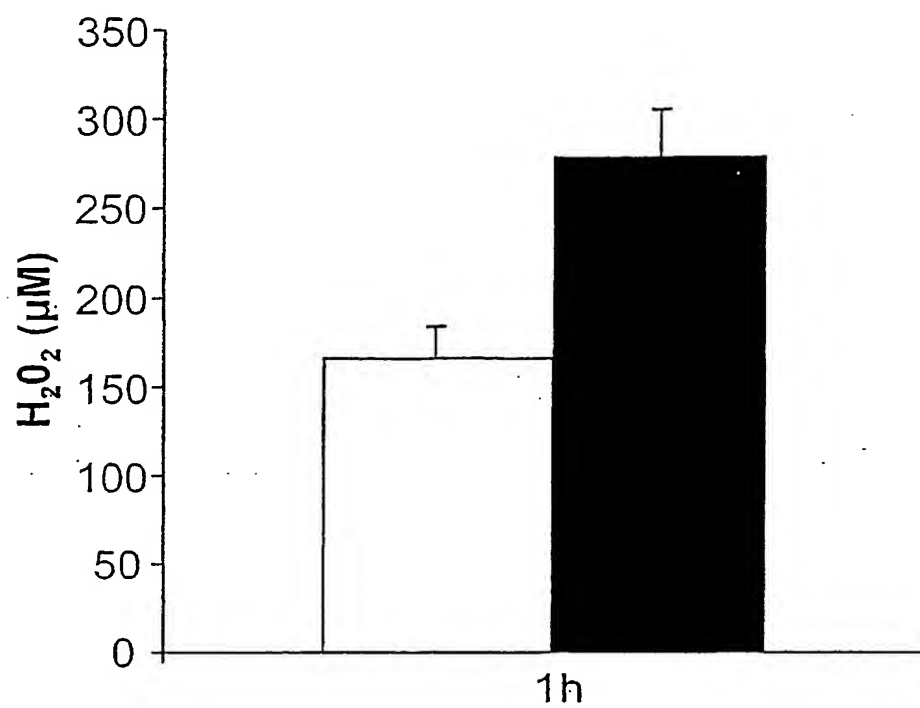


Fig.

6A



6B

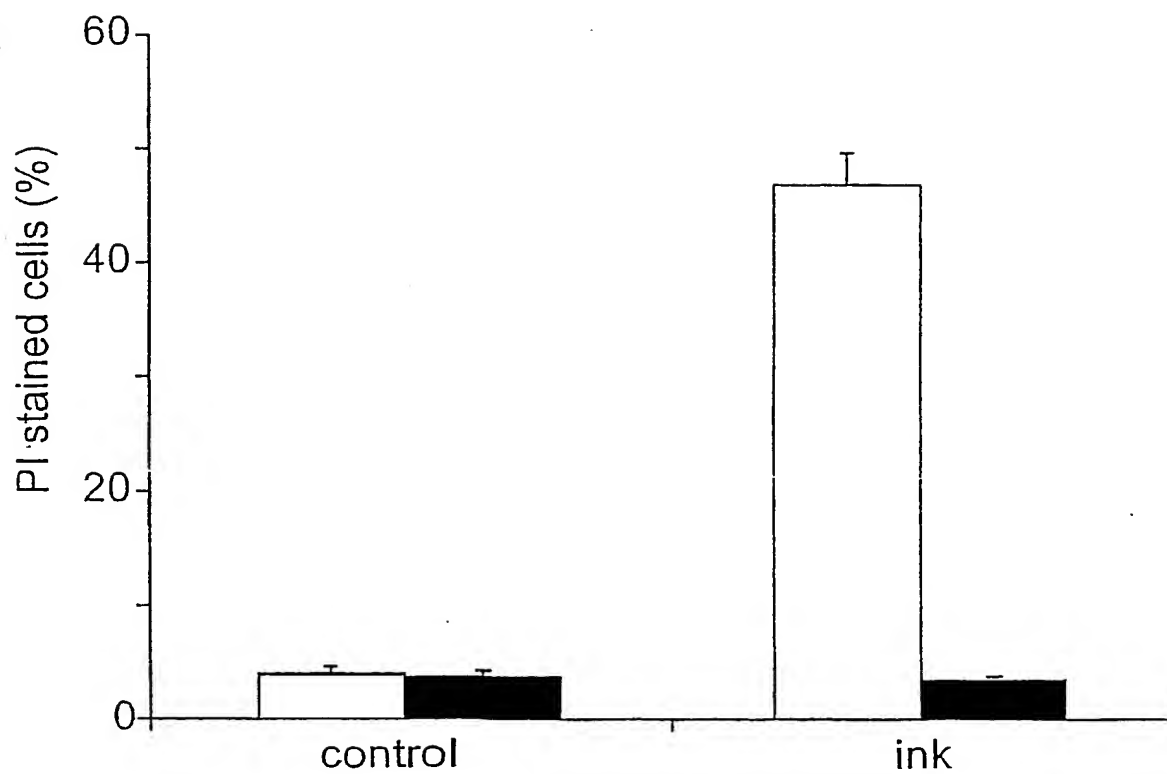
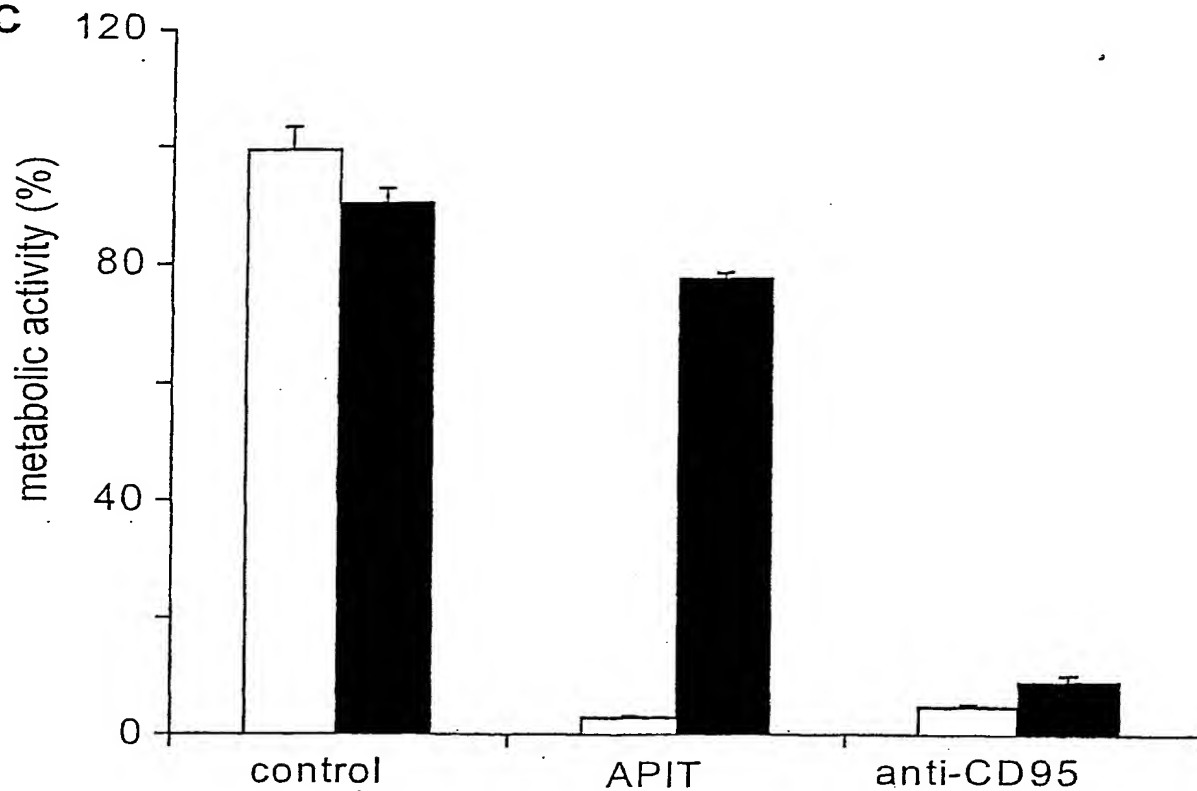


Fig.

6C



6D

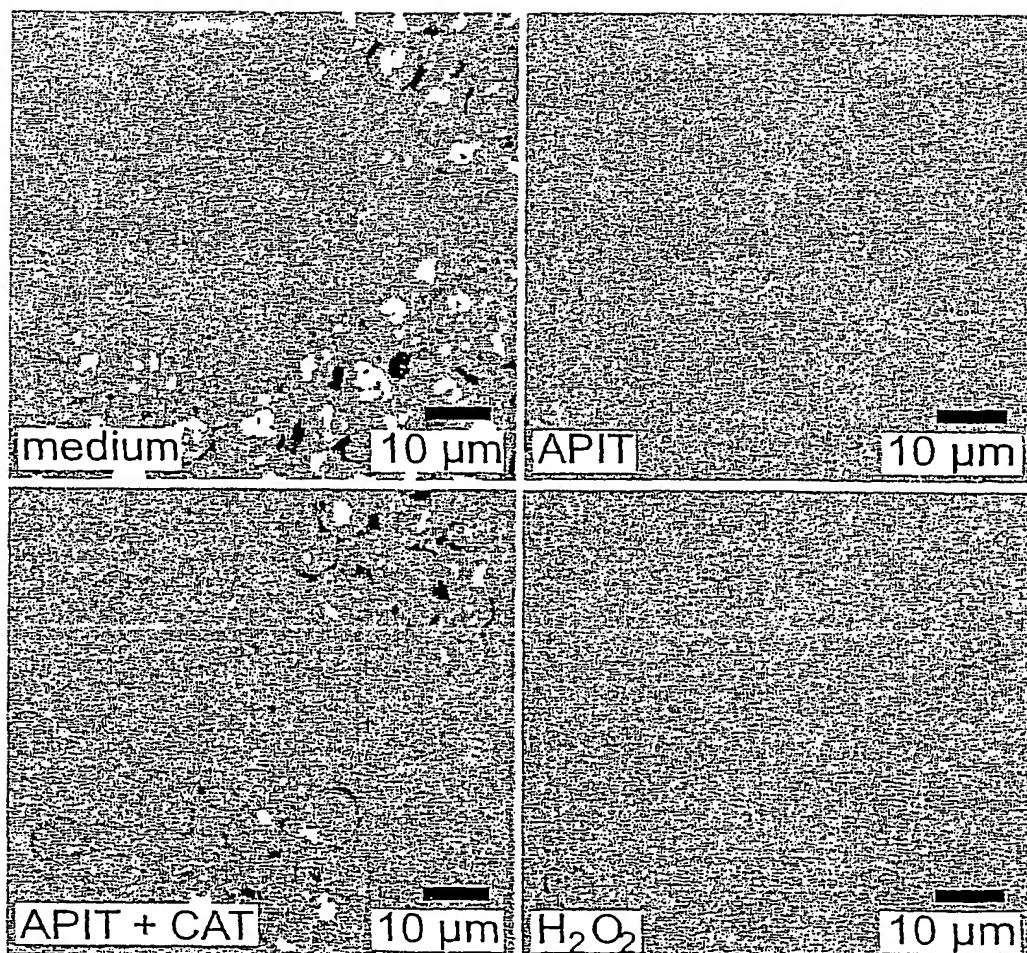


Fig. 6E

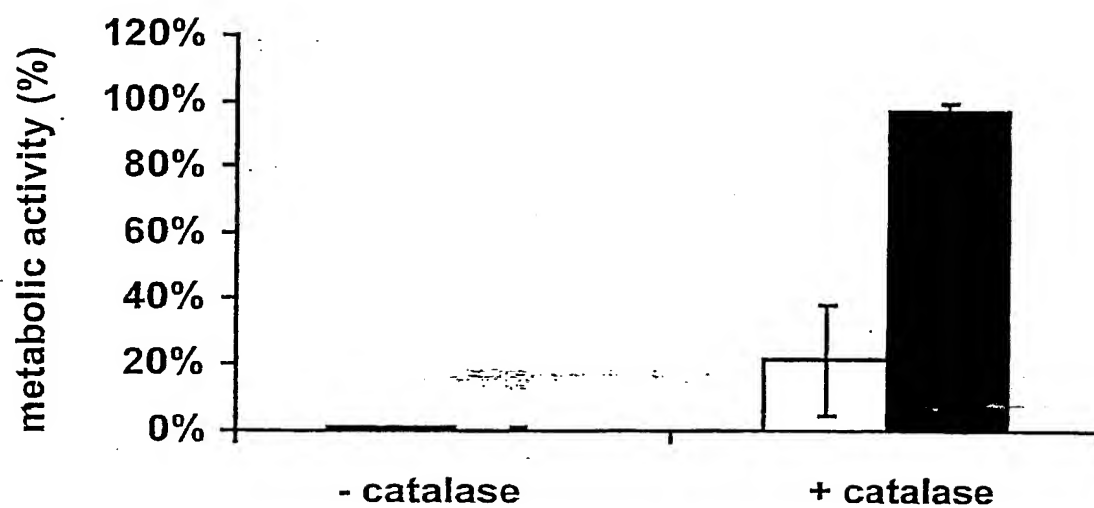
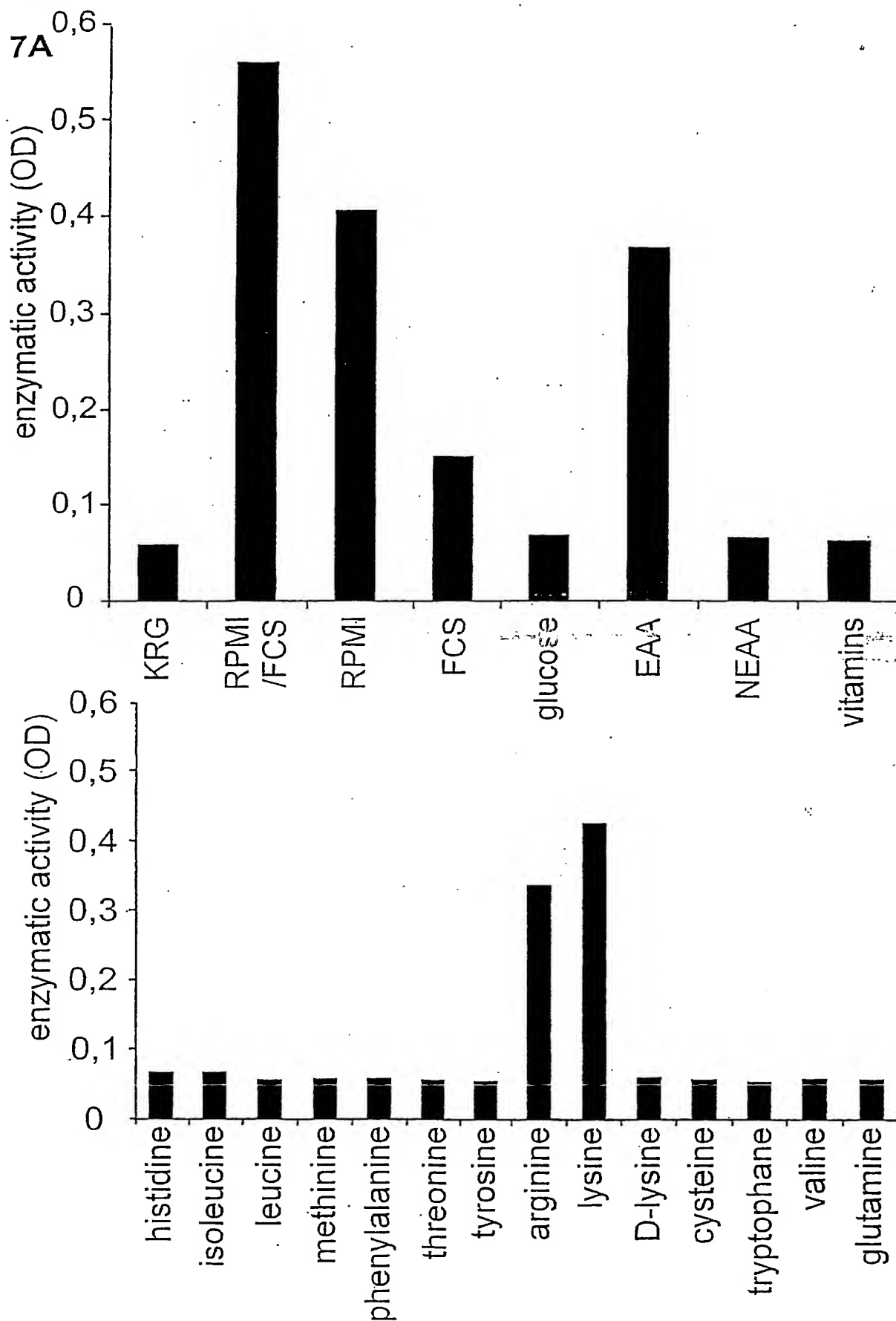


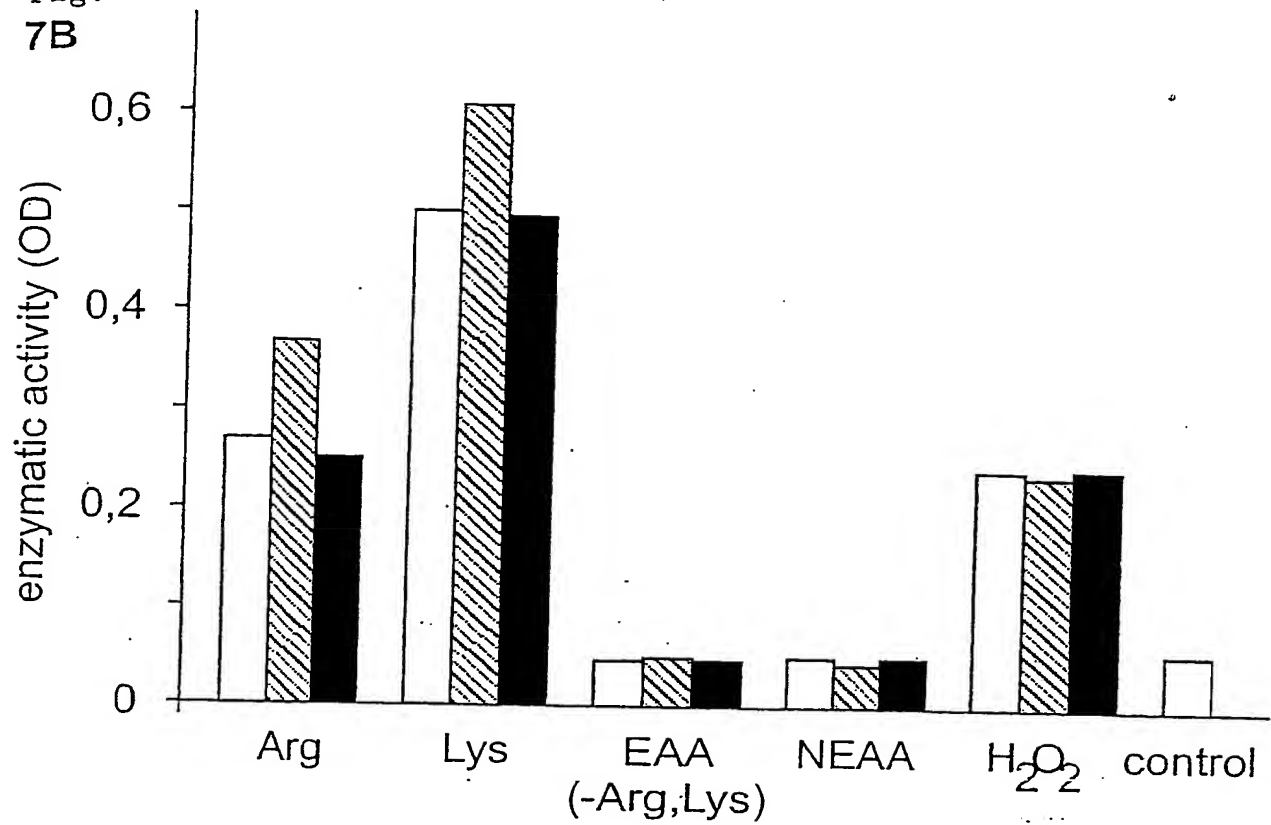
Fig.



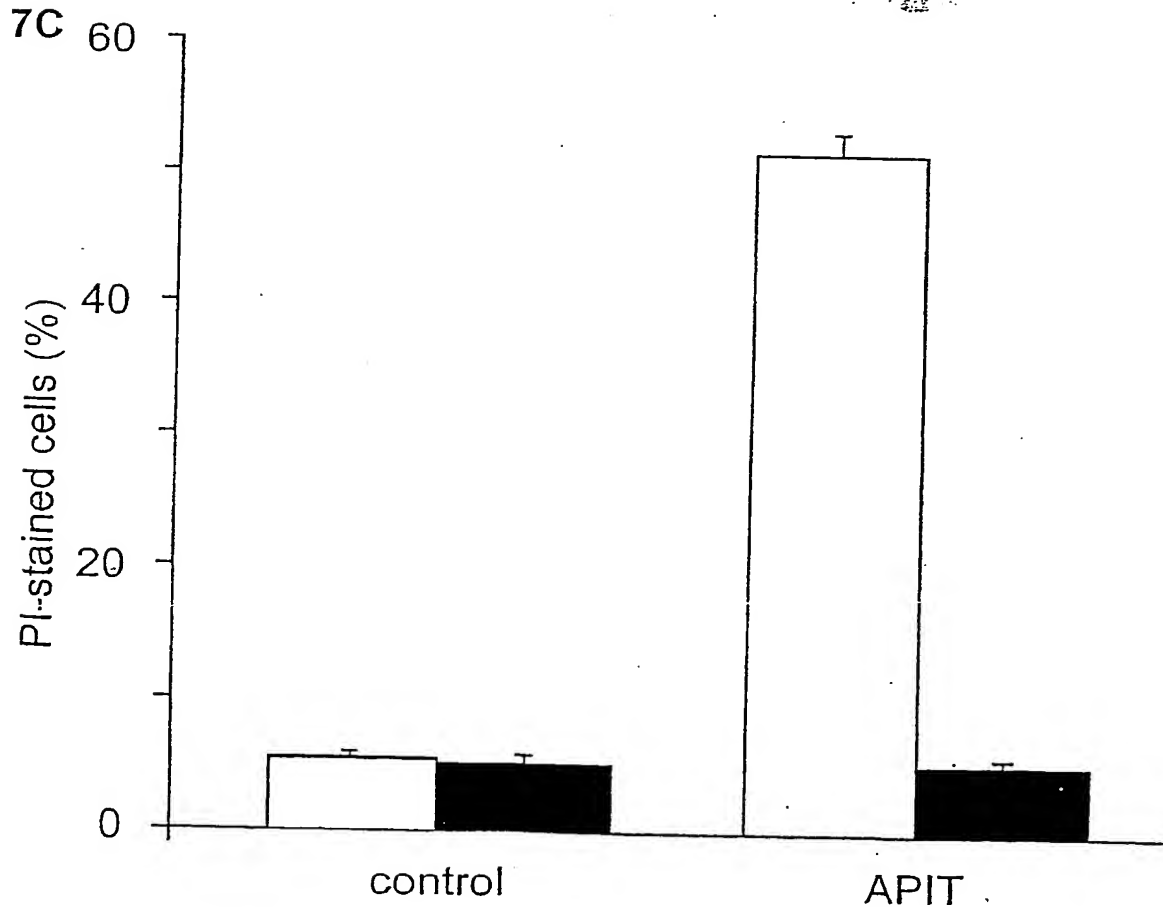
WO 2004/065415

Fig.

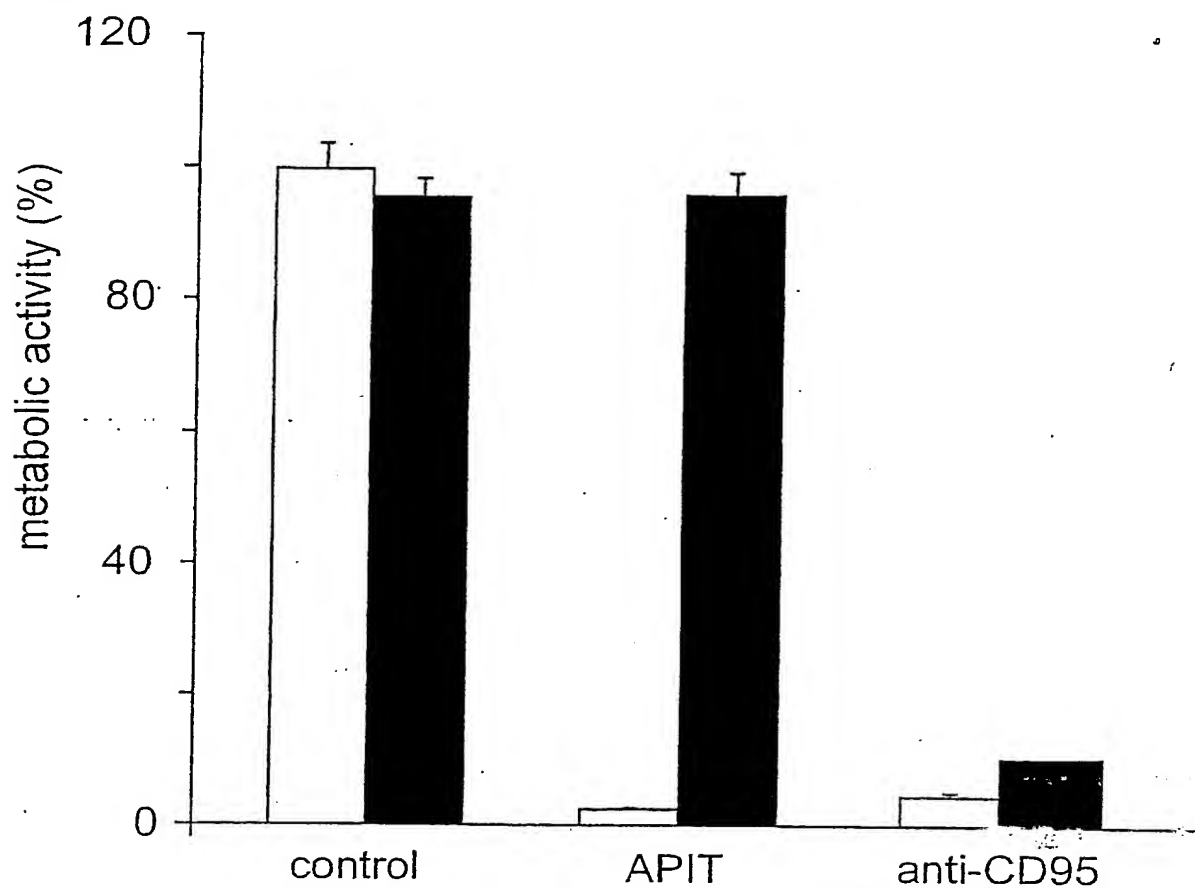
7B



7C



7D



7E

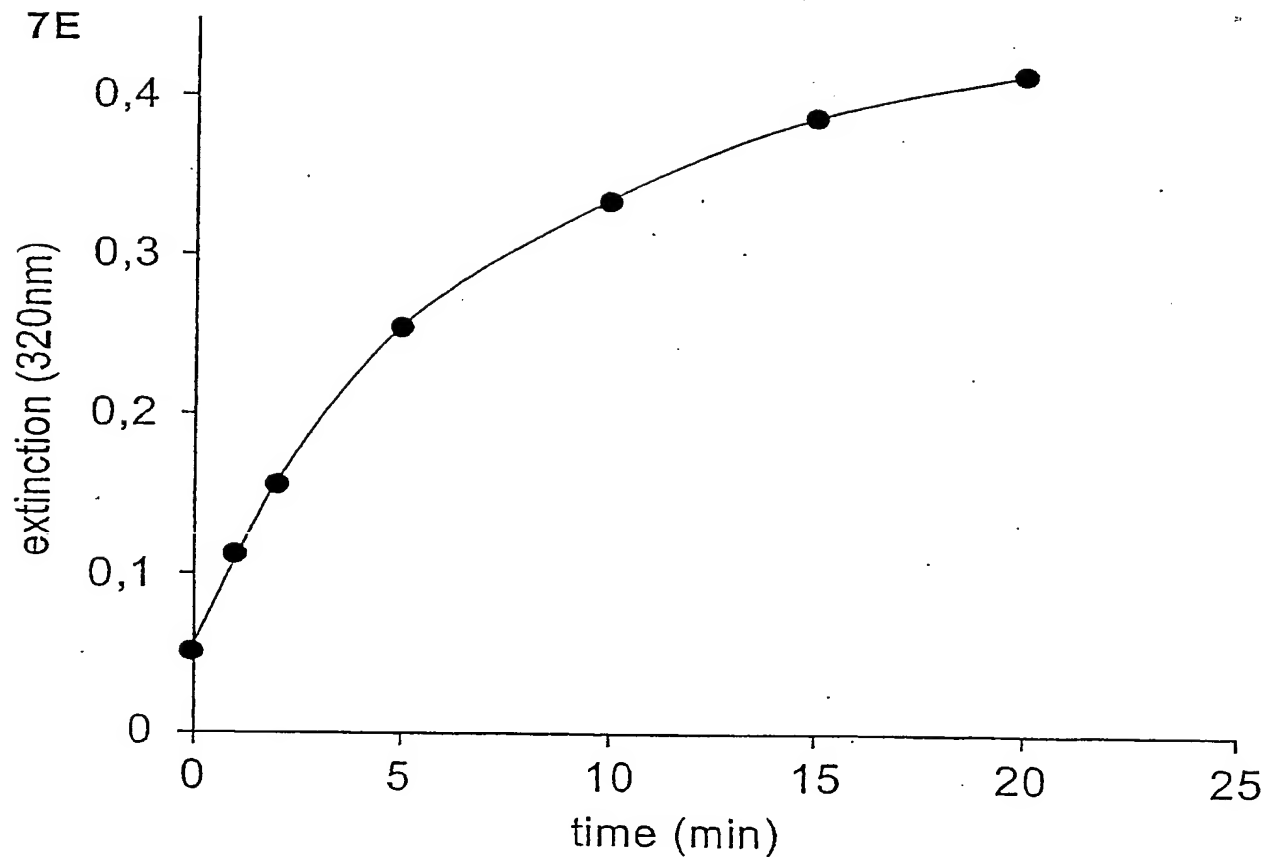
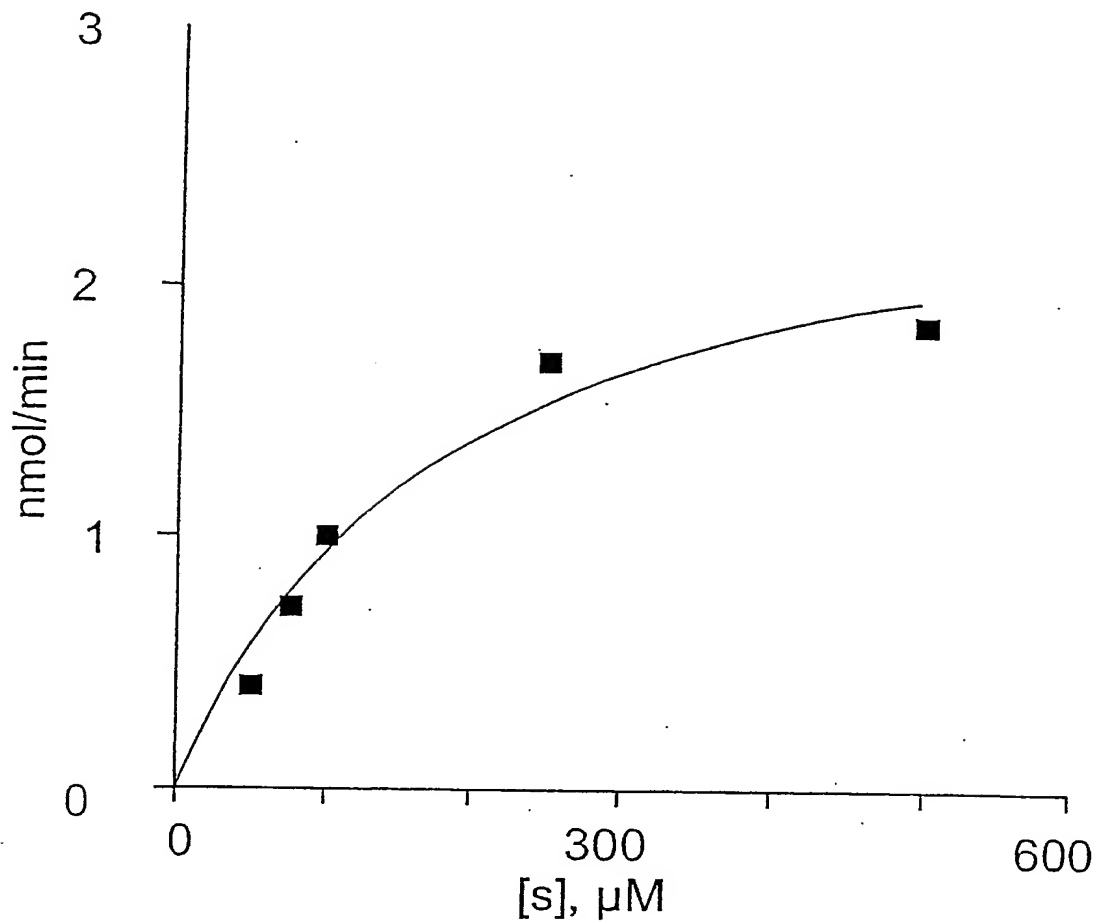


Fig.

7F



7G

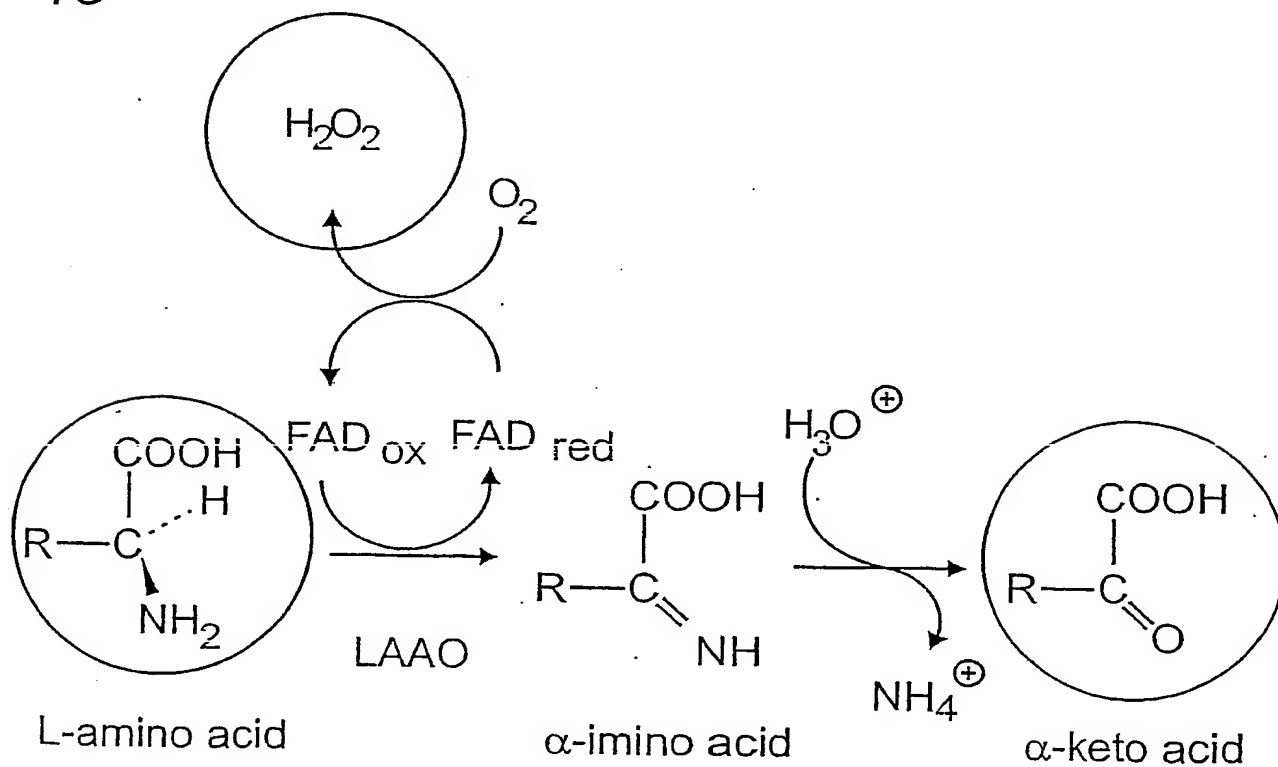


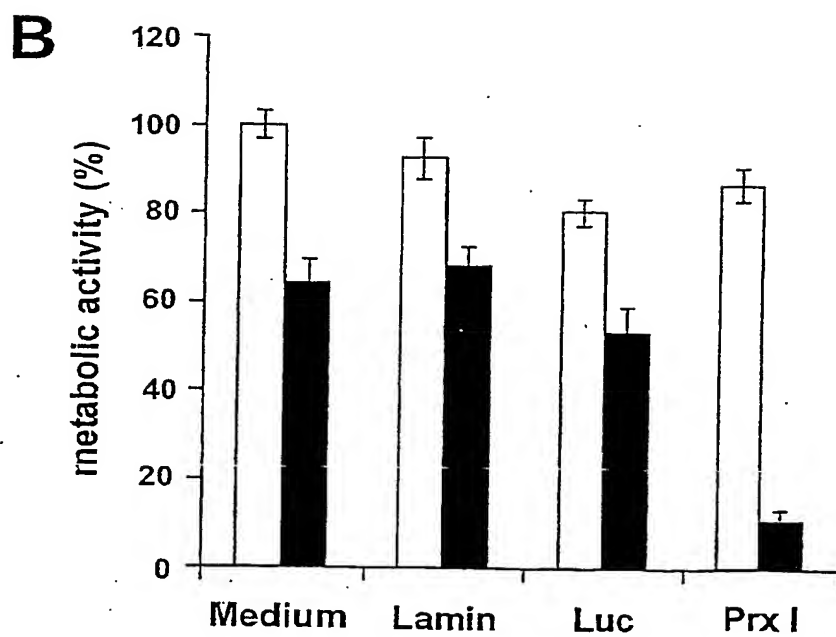
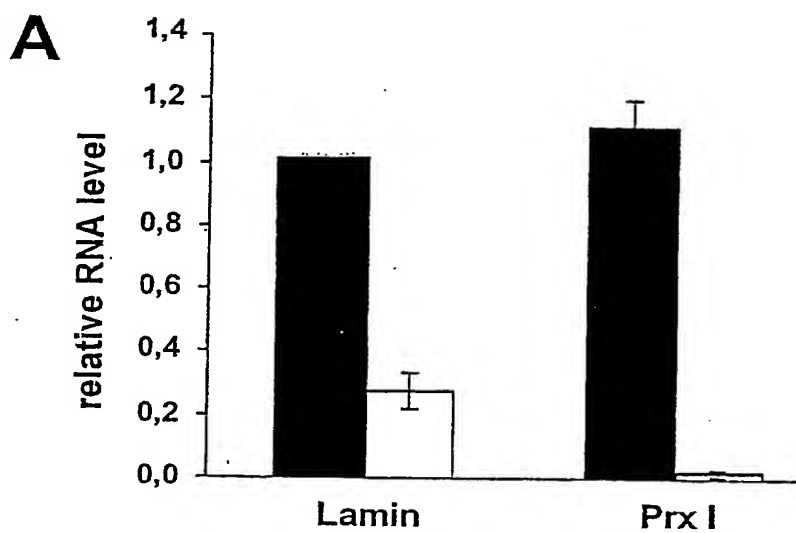
Fig. 8

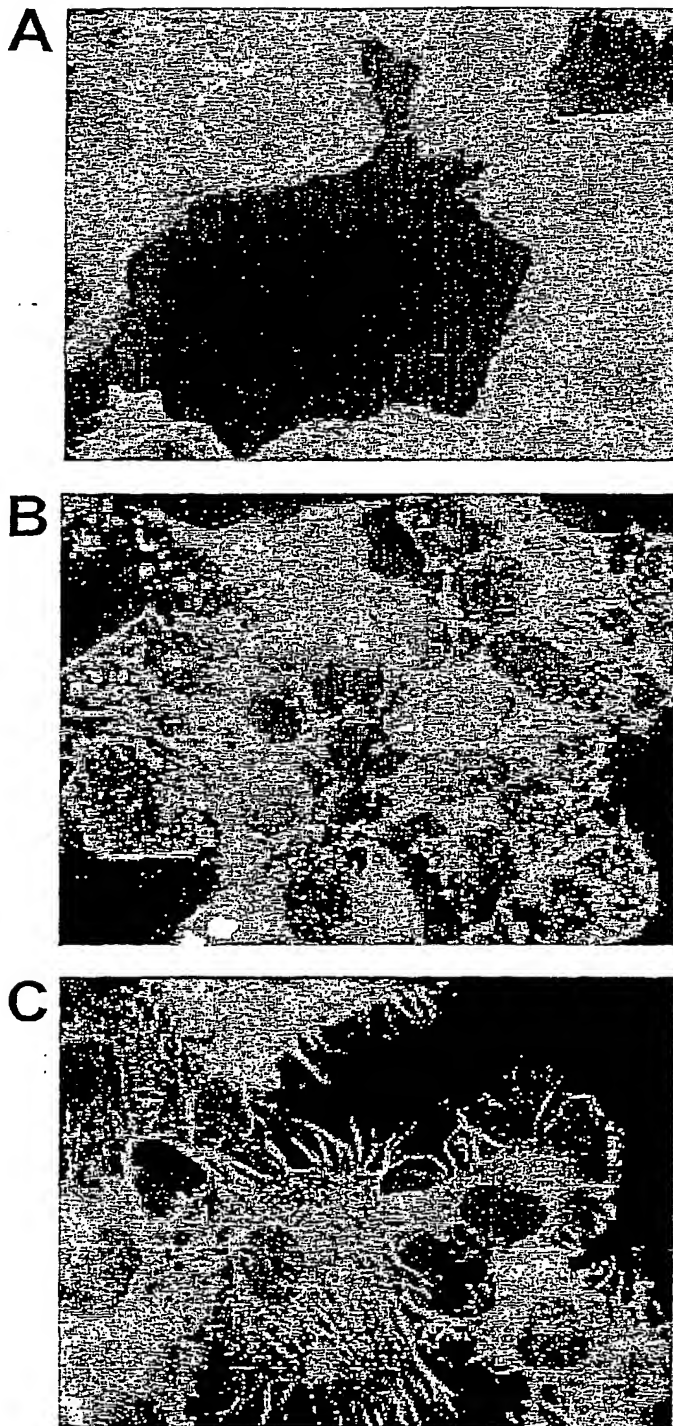
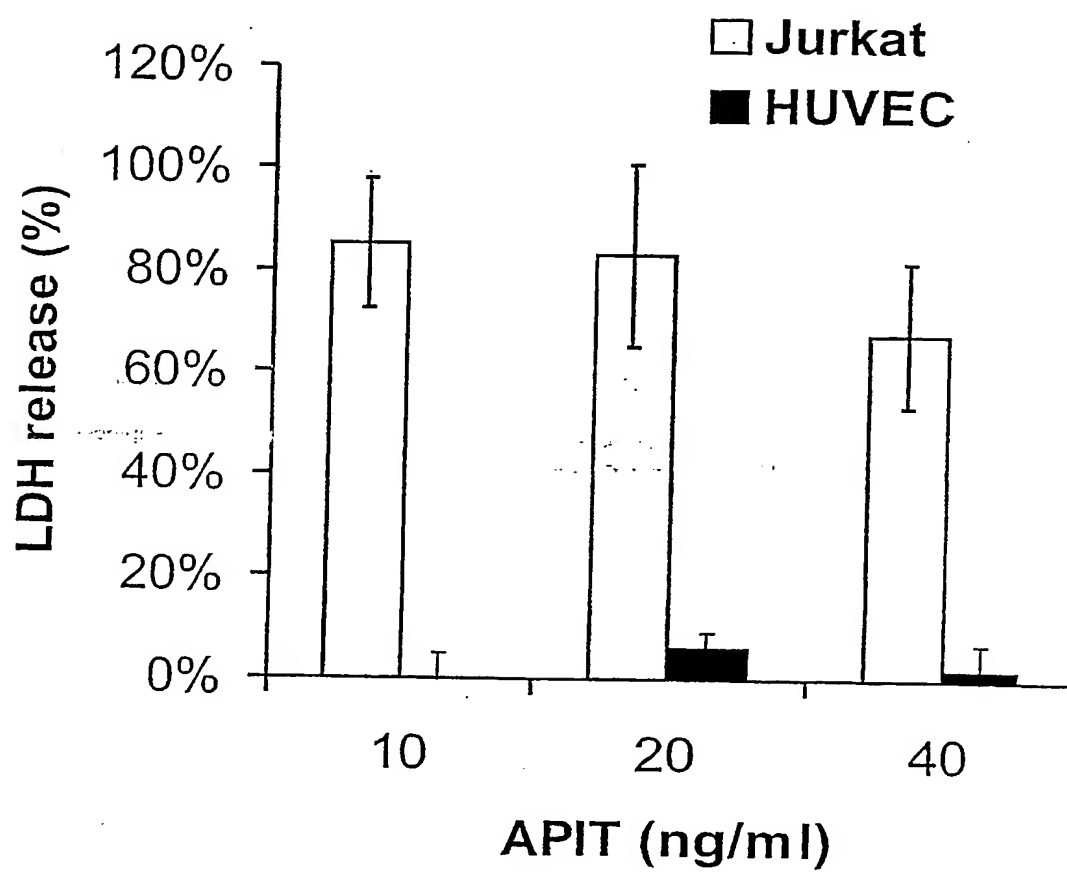
Fig. 9

Fig. 10

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